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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:31:42 ; Search time 61.6875 Seconds
(without alignments)
273.318 Million cell updates/sec

Title: US-09-913-927D-2

Perfect score: 262

Sequence: 1 MEQAPEDQGPQREPYNEWTL.....SEAVRHPPRIWLNLGQHIY 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 262 | 100.0 | 47 | 3 AAB10686 | Aab10686 HIV-1 reg |
| 2 | 262 | 100.0 | 60 | 7 ABR42471 | AbR42471 HIV viral |
| 3 | 262 | 100.0 | 79 | 2 AAR48961 | Aar48961 NL4-3 VPR |
| 4 | 262 | 100.0 | 96 | 2 AAR48963 | Aar48963 HIV VPR. |
| 5 | 262 | 100.0 | 96 | 2 AAW53040 | Aaw53040 HIV-1 pol |
| 6 | 262 | 100.0 | 96 | 3 AAB10049 | Aab10049 HIV-1 vpr |
| 7 | 262 | 100.0 | 96 | 3 AAB10685 | Aab10685 HIV-1 reg |
| 8 | 262 | 100.0 | 96 | 5 AAE16129 | Aae16129 Human imm |
| 9 | 262 | 100.0 | 96 | 5 ABP56175 | Abp56175 HIV-1 vir |
| 10 | 262 | 100.0 | 96 | 7 ADD01277 | Add01277 HIV-1 vpr |
| 11 | 262 | 100.0 | 96 | 8 Adf46812 | Adf46812 HIV-1 vpr |
| 12 | 262 | 100.0 | 96 | 8 ABM79669 | Abm79669 HIV-1 Vpr |
| 13 | 256 | 97.7 | 96 | 6 ABR55491 | AbR55491 Amino aci |
| 14 | 255 | 97.3 | 96 | 3 AAB69306 | Aab69306 HIV-1 non |
| 15 | 252 | 96.2 | 96 | 5 AAU80187 | Aau80187 HIV-1 Vpr |
| 16 | 251 | 95.8 | 78 | 2 AAW99828 | Aaw99828 HIV HXB2 |
| 17 | 251 | 95.8 | 96 | 2 AAW99823 | Aaw99823 HIV L68S |
| 18 | 251 | 95.8 | 96 | 2 AAW99824 | Aaw99824 HIV H71C |
| 19 | 251 | 95.8 | 96 | 2 AAW99821 | Aaw99821 HIV L64S |
| 20 | 251 | 95.8 | 96 | 2 AAW99826 | Aaw99826 HIV G75A |
| 21 | 251 | 95.8 | 96 | 2 AAW99820 | Aaw99820 HIV A59P |
| 22 | 251 | 95.8 | 96 | 2 AAW99825 | Aaw99825 HIV H71Y |
| 23 | 251 | 95.8 | 96 | 2 AAW99827 | Aaw99827 HIV C76S |
| 24 | 251 | 95.8 | 96 | 2 AAW99815 | Aaw99815 HIV Vpr w |
| 25 | 251 | 95.8 | 96 | 2 AAW99822 | Aaw99822 HIV L67S |

ALIGNMENTS

RESULT 1

AAB10686
ID AAB10686 standard; peptide; 47 AA.

XX AAB10686;

XX XX

DT 19-JAN-2001 (first entry)

XX HIV-1 regulatory virus protein R peptide svpr1-47.

XX Regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity;
KW structural analysis; cell cycle arrest.

XX Synthetic.

OS Human immunodeficiency virus 1.

XX Key Location/Qualifiers

PH Modified-site 47

FT /note= "C-terminal amide"

XX WO200049038-A2.

XX 24-AUG-2000.

XX 19-FEB-2000; 2000WO-DR000525.

XX 19-FEB-1999; 99DE-01008752.

XX 19-FEB-1999; 99DE-01008766.

XX (SCHU/) SCHUBERT U.

XX (HENK/) HENKLEIN P.

XX (WRAY/) WRAY V.

XX Schubert U, Henklein P, Wray V;

XX WPI; 2000-565367/52.

XX New synthetic peptides from the Vpr protein of human immune deficiency virus, useful e.g. for therapy and diagnosis, have good solubility in water.

XX Claim 3.2; Page 5; 35pp; German.

XX This invention describes novel synthetic peptides (i) derived from the regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-1) which have antiviral activity and can be used for gene therapy. (i) is used for therapeutic and/or diagnostic purposes, especially in biological assays, for development of serological tests or enzyme-linked

CC immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in
 CC blood), to raise specific antibodies and antisera (especially those
 CC reactive with specific epitopes), and as antiviral agents. (I) can also
 CC be used in screening for potential Vpr antagonists (i.e. compounds that
 CC modulate interaction of Vpr with cellular factors, transcription-
 CC activating properties of Vpr, transport of Vpr and its incorporation into
 CC viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-
 CC channel activities of Vpr). (I) is used to establish cell or animal
 CC models for studying pathogenicity of Vpr, for structural analysis of Vpr
 CC and its domains, for in vitro assembly of new vectors for gene therapy,
 CC in vitro or in vivo, for complementing the function of Vpr-defect mutants
 CC in cell cultures, and to reduce flexibility of Vpr induced by the N-
 CC terminal domain. Synthetic (I), are soluble in water and can be
 CC formulated as highly concentrated solutions (mmolar) without protein
 CC aggregation, so are well suited to analysis by nuclear magnetic
 CC resonance, X-ray or circular dichroism techniques. (I) adopt a folded
 CC structure, have biological activity comparable to that of viral Vpr, and
 CC can be produced, at high purity, on the milligram scale. This sequence
 CC represents the synthetic HIV-1 derived Vpr peptide sVpr1-47 which is used
 CC in the method of the invention

XX
 SQ Sequence 47 AA;

Query Match 100.0%; Score 262; DB 3; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.9e-26;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLELLELSEAVRHPFRIWHLNLGHQIY 47
 |||||
 Db 1 MEQAPEDQGPQREPYNEWTLLELLELSEAVRHPFRIWHLNLGHQIY 47

RESULT 2
 ABR42471
 ID ABR42471 standard; protein; 60 AA.

XX
 AC ABR42471;
 DT 11-AUG-2003 (first entry)
 XX
 DE HIV viral protein R (aa-160).
 KW HIV; viral protein R; Vpr; lentiviral R protein; anti-HIV; virucide.
 XX
 OS Human immunodeficiency virus.

XX
 FH Key Location/Qualifiers
 FT Region 17..29
 FT /note= "alpha-helix 1"
 FT Region 36..47
 FT /note= "alpha-helix-2"

XX WO2003038056-A2.

XX
 PN 08-MAY-2003.

XX 31-OCT-2002; 2002WO-US035110.

XX 02-NOV-2001; 2001US-0350168P.

XX (REGC) UNIV CALIFORNIA.

XX Sherman M, Greene WC, Schubert U, Wray V, Tessmer U, Henklein P;
 PI Bruns K;

XX WPI; 2003-468412/44.

XX Identifying an agent that induces Vpr loss in a lentivirus-infected cell,
 PT useful for treating lentiviral infections by determining the effect of
 PT the test agent contacted with a cell that produces Vpr protein on the
 PT level of Vpr in the cell.

XX Example 5; Fig 4; 44pp; English.

XX
 CC The present sequence is that of amino acids 1-60 of HIV viral protein R
 CC (Vpr, also called lentiviral R protein). Vpr is incorporated into the HIV
 CC virion and helps to target the viral preintegration complex to the
 CC nucleus in nondividing cells through its nuclear localisation signal. It
 CC is also responsible for arresting HIV infected cells in the G2 phase of
 CC the cell cycle, which results in increased virus production. The
 CC invention provides methods for identifying compounds that induce loss of
 CC Vpr in a eukaryotic cell, and methods for identifying compounds that
 CC inhibit a peptidyl-prolyl cis/trans isomerase activity of a protein that
 CC catalyses cis-trans isomerization of cis-peptidylprolyl bonds in Vpr.
 CC Such compounds are useful for treating lentiviral infections, including
 CC HIV infections

XX Sequence 60 AA;

Query Match 100.0%; Score 262; DB 7; Length 60;
 Best Local Similarity 100.0%; Pred. No. 3.8e-26;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLELLELSEAVRHPFRIWHLNLGHQIY 47
 |||||
 Db 1 MEQAPEDQGPQREPYNEWTLLELLELSEAVRHPFRIWHLNLGHQIY 47

RESULT 3
 AAR48961
 ID AAR48961 standard; protein; 79 AA.

XX
 AC AAR48961;

XX 25-MAR-2003 (revised)

DT 12-SEP-1994 (first entry)

XX NL4-3 VPR N-terminal peptide.

XX HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;
 KW naturally occurring virus; NOV; translation; replication; infectivity;
 KW hepatitis B; HIV-2; SIV; flip-over PCR.

XX Synthetic.

XX WO9403596-A1.

XX 17-FEB-1994.

XX 30-JUL-1993; 93WO-US007179.

XX 30-JUL-1992; 92US-00921104.

XX (UYHA-) UNIV HAWAII.

XX Hu W, Wang J;

XX WPI; 1994-065685/08.

XX N-PSDB; AAQ57688.

XX New antisense viruses and anti-sense-ribozyme viruses - used for treating
 PT or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.

XX Disclosure; Page 108; 167pp; English.

XX This sequence is encoded by a PCR fragment of NL4-3 and represents the N-
 CC terminal peptide fragment of the full length VPR protein. The DNA
 CC encoding this fragment was ligated into ClaI/SalI digested pX and the
 CC corresponding plasmid was used to produce the antisense virus of the
 CC invention. Antisense or truncated RNAs expressed by these viruses bind to
 CC the mRNAs expressed by the naturally occurring viruses (NOVs) and prevent
 CC the mRNAs from being translated into proteins, thereby preventing the NOV
 CC from replicating. The antisense viruses maintain the infectivity of the
 CC NOVs, allowing antisense RNAs to reach the mRNAs of the natural viruses.
 CC Antisense viruses such as these may be used for treating or preventing a
 CC viral infection, particularly HIV-1, HIV-2 or SIV infection or hepatitis

CC B infection. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 79 AA;
SQ Query Match 100.0%; Score 262; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 5.3e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRILWHLNLGHQIY 47
Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRILWHLNLGHQIY 47

RESULT 4
AAR48963
ID AAR48963 standard; protein; 96 AA.

XX AAR48963;
AC AAR48963;
XX 25-MAR-2003 (revised)
DT 12-SEP-1994 (first entry)
XX HIV VPR.
XX HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;
KW naturally occurring virus; NOV; translation; replication; infectivity;
KW hepatitis B; HIV-2; SIV; flip-over PCR.
XX Synthetic.

XX OS
XX PN W09403596-A1.
XX 17-FEB-1994.
XX 30-JUL-1993; 93WO-US007179.
XX 30-JUL-1992; 92US-00921104.
XX (UYHA-) UNIV HAWAII.
XX Hu W, Wang J;
XX WPI; 1994-065685/08.
DR N-PSDB; AAQ48962.
XX New antisense viruses and anti-sense-ribozyme viruses - used for treating
PT or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.
XX Disclosure; Page 111; 167pp; English.

XX This sequence represents the "perfect" VPR protein encoded by the PCR
CC fragment of pX-CS which encodes the truncated gag gene and the "perfect"
CC vpr gene. The cDNA fragment encoding this protein was used to produce the
CC antisense virus of the invention. Antisense or truncated RNAs expressed
CC by these viruses bind to the mRNAs expressed by the naturally occurring
CC viruses (NOVs) and prevent the mRNAs from being translated into proteins,
CC thereby preventing the NOV from replicating. The antisense viruses
CC maintain the infectivity of the NOVs, allowing antisense RNAs to reach
CC the mRNAs of the natural viruses. Antisense viruses such as these may be
CC used for treating or preventing a viral infection, particularly HIV-1,
CC HIV-2 or SIV infection or hepatitis B infection. (Updated on 25-MAR-2003
CC to correct PN field.)

SQ Sequence 96 AA;
Query Match 100.0%; Score 262; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.6e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRILWHLNLGHQIY 47
Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRILWHLNLGHQIY 47

RESULT 5
AAW53040
ID AAW53040 standard; peptide; 96 AA.

XX AAW53040;
AC AAW53040;
XX 17-OCT-2003 (revised)
DT 17-JUL-1998 (first entry)
XX HIV-1 polypeptide.

XX Recombinant plant virus; HIV-1; protein production; immunisation;
KW fusion capsid protein; alfalfa mosaic virus; ilarvirus; pathogen;
KW rhabdovirus.

XX OS Human immunodeficiency virus 1.
XX PN W09808375-A1.
XX 05-MAR-1998.

XX 28-AUG-1997; 97WO-US015200.
XX 28-AUG-1996; 96US-00704856.
XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Koprowski H, Hooper DC, Yusibov V, Modelska A;
XX WPI; 1998-179070/16.

XX Production of poly:peptide(s), particularly for use in vaccines - by
PT expression as fusion proteins with plant virus capsid protein in plant
PT cells infected with virus.

XX Disclosure; Page 4; 63pp; English.

XX This sequence is a HIV-1 polypeptide that can be used in a recombinant
CC plant virus used in the process of the invention. The process is for
CC administering a polypeptide to an animal comprising: (a) infecting a
CC plant cell with recombinant plant virus nucleic acid that will be
CC processed in a plant cell to produce a fusion capsid protein (FCP), the
CC FCP comprises a plant virus capsid protein (PVCp) and a polypeptide that
CC is not a PVCp, the PVCp being an alfalfa mosaic virus (AlMV) capsid
CC protein (CP) or ilarvirus CP thereby creating a infected cell; (b)
CC cultivating the infected cell, or a derivative cell derived from the
CC infected cell, under conditions where the infected cell or derivative
CC cell makes the FCP; and (c) administering the FCP or a portion to an
CC animal. The recombinant plant virus can also be used for production of
CC polypeptides. The method is used particularly for the production of
CC polypeptides which can be used for immunisation against pathogens such as
CC rhabdovirus or HIV. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 96 AA;

Query Match 100.0%; Score 262; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.6e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRILWHLNLGHQIY 47
Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHFPRILWHLNLGHQIY 47

RESULT 6
AAB10049
ID AAB10049 standard; protein; 96 AA.

XX AAB10049;
AC AAB10049;
XX 12-SEP-2003 (revised)
DT 02-NOV-2000 (first entry)

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XX HIV-1 vpr protein.
DE
XX
XX Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic; gene therapy;
KW treatment; infectious disease; HIV; AIDS; neoplasm; carcinoma; melanoma;
KW vpr protein.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX EF1006196-A2.
PN
XX
XX 07-JUN-2000.
PD
XX
XX 25-NOV-1999; 99EP-00250415.
PF
XX
XX 26-NOV-1998; 98DE-01056463.
PR
XX
XX (PETT-) PETTE INST HEINRICH.
PA
XX
XX Von Laer MD;
PI
XX
XX WPI; 2000-378268/33.
DR
XX
XX N-PSDB; AAA40298, AAB10053, AAB10054.
DR
XX
XX New retroviral packing cell useful as pharmaceutical carrier in gene
PT therapy for treatment of HIV and neoplasms, comprises retroviral genes
PT and glycoproteins.
PT
XX
XX Disclosure; Page 44; 69pp; German.
PS
XX
XX This invention describes a novel retroviral packing cell (I), comprising
CC the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV
CC coding gene gp or a part of these. The products of the invention have
CC anti-HIV and cytostatic activity and can be used for gene therapy. (I) is
CC useful for in vitro infection of cells, especially hematopoietic stem
CC cells, for expression of transgenes in cells and as a pharmaceutical
CC carrier for gene therapy. (I) is therefore useful in the treatment of
CC infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and
CC other diseases. This sequence represents the Human immunodeficiency virus
CC (HIV-1) vpr protein described in the method of the invention. (Updated on
CC 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 96 AA;
Query Match 100.0%; Score 262; DB 3; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.6e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQAPEDQGQPREPYNEWTLLELLELKSEAVRHFPRFWLHNLGQHIY 47
DB 1 MEQAPEDQGQPREPYNEWTLLELLELKSEAVRHFPRFWLHNLGQHIY 47
RESULT 7
AAB10685
ID AAB10685 standard; peptide; 96 AA.
XX
XX AAB10685;
AC
XX
XX 19-JAN-2001 (first entry)
DT
XX
XX HIV-1 regulatory virus protein R peptide sVpr1-96.
DE
XX
XX Regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity;
KW structural analysis; cell cycle arrest.
KW
XX
XX Synthetic.
OS
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO200049038-A2.
PN
XX
XX 24-AUG-2000.
PD
XX
XX

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PF 19-FEB-2000; 2000WO-DE000525.
XX
PR 19-FEB-1999; 99DE-01008752.
PR 19-FEB-1999; 99DE-01008766.
XX
PA (SCHU/) SCHUBERT U.
PA (HENK/) HENKLEIN P.
PA (WRAY/) WRAY V.
XX
PI Schubert U, Henklein P, Wray V;
XX
XX WPI; 2000-565367/52.
DR
XX
XX New synthetic peptides from the Vpr protein of human immune deficiency
PT virus, useful e.g. for therapy and diagnosis, have good solubility in
PT water.
PT
XX
XX Claim 3.1; Page 5; 35pp; German.
PS
XX
XX This invention describes novel synthetic peptides (I) derived from the
CC regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-
CC 1) which have antiviral activity and can be used for gene therapy. (I) is
CC used for therapeutic and/or diagnostic purposes, especially in biological
CC assays, for development of serological tests or enzyme-linked
CC immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in
CC blood), to raise specific antibodies and antisera (especially those
CC reactive with specific epitopes), and as antiviral agents. (I) can also
CC be used in screening for potential Vpr antagonists (i.e. compounds that
CC modulate interaction of Vpr with cellular factors, transcription-
CC activating properties of Vpr, transport of Vpr and its incorporation into
CC viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-
CC channel activities of Vpr). (I) is used to establish cell or animal
CC models for studying pathogenicity of Vpr, for structural analysis of Vpr
CC and its domains, for in vitro assembly of new vectors for gene therapy,
CC in vitro or in vivo, for complementing the function of Vpr-defect mutants
CC in cell cultures, and to reduce flexibility of Vpr induced by the N-
CC terminal domain. Synthetic (I), are soluble in water and can be
CC formulated as highly concentrated solutions (mmolar) without protein
CC aggregation, so are well suited to analysis by nuclear magnetic
CC resonance, X-ray or circular dichroism techniques. (I) adopt a folded
CC structure, have biological activity comparable to that of viral Vpr, and
CC can be produced, at high purity, on the milligram scale. This sequence
CC represents the synthetic HIV-1 derived Vpr peptide sVpr1-96 which is used
CC in the method of the invention
XX
SQ Sequence 96 AA;
Query Match 100.0%; Score 262; DB 3; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.6e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQAPEDQGQPREPYNEWTLLELLELKSEAVRHFPRFWLHNLGQHIY 47
DB 1 MEQAPEDQGQPREPYNEWTLLELLELKSEAVRHFPRFWLHNLGQHIY 47
RESULT 8
AAB16129
ID AAB16129 standard; protein; 96 AA.
XX
XX AAB16129;
AC
XX
XX 29-AUG-2003 (revised)
DT
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Human immunodeficiency virus type 1 (HIV-1) sVpr protein.
DE
XX
XX Human immunodeficiency virus type 1; HIV-1; auxiliary protein; cancer;
KW Vpr protein; regulatory protein; pathogen; cell proliferation; therapy;
KW dysregulated cell growth; hyperproliferative cell disorder; malignancy;
KW radiation therapy; psoriasis; transgene expression; immune response;
KW cytostatic; apoptotic.
KW
XX

```

OS Human immunodeficiency virus 1.

XX Key Location/Qualifiers

PH Region 17..29

FT /label= Alpha_1_helix

FT Region 36..47

FT /label= Alpha_2_helix

FT Region 53..78

FT /label= Alpha_3_helix

XX WO200190159-A2.

XX 29-NOV-2001.

XX 23-MAY-2001; 2001WO-US016943.

XX 23-MAY-2000; 2000US-0206610P.

PR 09-FEB-2001; 2001US-0267827P.

PR 20-APR-2001; 2001US-00839329.

XX (GLAD-) GLADSTONE INST J DAVID.

PA (SCHU/) SCHUBERT U.

PA (HENK/) HENKLEIN P.

XX Schubert U, Henklein P, Sherman MP, Greene WC, De Noronha CMC;

XX WPI; 2002-083087/11.

XX Delivering molecule into cell for inhibiting cell proliferation and

PT killing target cell, comprises contacting cell with Vpr polypeptide,

PT regulatory protein encoded by HIV type 1, alone or conjugated to

PT molecule.

XX Example 1; Fig 1A; 72pp; English.

XX The present invention relates to compositions comprising Vpr polypeptides

CC conjugated to a therapeutic molecule. Vpr polypeptides are regulatory or

CC auxiliary proteins encoded by a lentivirus, human immunodeficiency virus

CC type 1 (HIV-1). The invention also relates to a method for delivering a

CC molecule into a cell which comprises contacting the cell with a conjugate

CC comprising a Vpr polypeptide conjugated to the molecule. The method is

CC useful for delivering a polypeptide, polynucleotide (DNA or RNA) or a

CC toxin into a cell, preferably a cancer cell, or a cell infected with a

CC pathogen such as lentivirus, HIV or retrovirus, bacterium or a parasite.

CC Compositions comprising Vpr polypeptide conjugated to a toxin is useful

CC for killing a cancer cell or a cell infected with a pathogen where the

CC toxin is further conjugated to a regulatory molecule and the contact with

CC the target cell exerts an effect on the regulatory molecule that results

CC in activation of the toxin. The method is useful for inhibiting cell

CC proliferation and treating a disorder associated with dysregulated cell

CC growth in a subject. Vpr polypeptides when administered alone are useful

CC for increasing sensitivity to radiation therapy in a subject undergoing

CC radiation therapy. The method can also be used to treat hyperproliferative cell

CC disorders such as malignancies, psoriasis and other disorders associated

CC with dysregulated cell growth. Vpr polypeptides conjugated to a

CC regulatory moiety is useful for modulating the expression of a transgene

CC in a cell. Vpr polypeptides alone or conjugated to an antigen is useful

CC for increasing an immune response. The present sequence is synthetic Vpr

CC (sVpr) protein from HIV-1. (Updated on 29-AUG-2003 to standardise OS

CC field)

XX

SQ Sequence 96 AA;

Query Match 100.0%; Score 262; DB 5; Length 96;

Best Local Similarity 100.0%; Pred. No. 6.6e-26;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHFPRWLHNLGHQHY 47

Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHFPRWLHNLGHQHY 47

RESULT 9

ABP56175

ID ABP56175 standard; peptide; 96 AA.

AC ABP56175;

XX 29-AUG-2003 (revised)

DT 28-MAR-2003 (first entry)

XX HIV-1 viral protein R (Vpr) amino acid sequence.

XX Mitochondrial membrane permeabilisation; mitochondrion; PTPC;

KW permeability transition pore complex; virucide; neuroprotective;

KW vasotropic; cytostatic; infection; cell death regulation; apoptosis;

KW mitochondrial permeability transition pore complex modulator; cancer;

KW apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.

XX Human immunodeficiency virus 1.

XX WO200261105-A2.

XX 08-AUG-2002.

XX 01-FEB-2002; 2002WO-EF001633.

XX 02-FEB-2001; 2001US-0265594P.

XX (INSP) INST PASTEUR.

XX (CNRS) CENT NAT RECH SCI.

XX Edelman L, Jacotot E, Briand J;

XX WPI; 2002-619260/66.

XX New chimeric bifunctional molecules that target specific cells and

PT regulate the apoptosis function of the permeability transition pore

PT complex of the mitochondria, useful for treating or preventing e.g.

PT cancer or ischemia.

XX Disclosure; Page 13; 76pp; English.

XX The present invention describes a chimeric bifunctional molecule (I)

CC comprising at least a first functional molecule covalently linked to a

CC second functional molecule, which is able to modulate the activity of the

CC permeability transition pore complex (PTPC) of the mitochondria. (I) has

CC the function of specifically targeting and entering a tissue cell

CC population. The second functional molecule has the function of

CC specifically targeting, and inducing or preventing the death of the cells

CC by apoptosis by regulating the opening or the closing of the PTPC of the

CC mitochondria or its fragment. (I) has virucide, neuroprotective,

CC vasotropic and cytostatic activities, and can be used as a mitochondrial

CC permeability transition pore complex (PTPC) modulator. (I) is useful for

CC treating or preventing a pathological infection or disease. (I) is also

CC useful for regulating cell death regulatory molecules, specifically the

CC apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia,

CC neurodegenerative diseases, fulminant hepatitis or viral infections. The

CC present sequence represents the HIV-1 viral protein R (Vpr) amino acid

CC sequence, which is given in the exemplification of the present invention.

CC (Updated on 29-AUG-2003 to standardise OS field)

XX

SQ Sequence 96 AA;

Query Match 100.0%; Score 262; DB 5; Length 96;

Best Local Similarity 100.0%; Pred. No. 6.6e-26;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHFPRWLHNLGHQHY 47

Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHFPRWLHNLGHQHY 47

RESULT 10

ADD01277

ID ADD01277 standard; protein; 96 AA.

XX ADD01277;
 AC 01-JAN-2004 (first entry)
 DT HIV-1 Vpr CypA protein binding motif.
 DE
 XX
 XX lentivirus protein R; Vpr; inhibitor; cellular chaperone; folding;
 KW stability; cyclophilin A; CypA; cell-cycle arrest; apoptosis;
 KW glucocorticoid receptor coactivation; anti-HIV; neurotropic; nephrotropic;
 KW antileptic; antiretroviral; AIDS; infection; HIV-induced dementia;
 KW lipodystrophy syndrome; lipid metabolism; HIV-associated nephropathy.
 XX
 OS Human immunodeficiency virus 1.
 XX
 XX WO2003038032-A2.
 PN
 XX
 XX 08-MAY-2003.
 PD
 XX
 XX 25-OCT-2002; 2002WO-DE004052.
 PF
 XX 25-OCT-2001; 2001DE-01053902.
 PR
 XX (MEDI-) MEDICIS VENTURES MANAGEMENT GMBH.
 PA
 XX Will H, Tessmer U, Bruns K;
 PI WPI; 2003-430506/40.
 DR
 XX
 XX Agent for inhibiting lentivirus Vpr protein, useful for treatment and
 PT prevention of infection by human immune deficiency virus, is inhibitor of
 PT chaperone enzyme.
 PT
 XX
 XX Disclosure; Fig 4; 41pp; German.
 XX
 XX This invention describes a novel agent (A), for inhibiting the primate
 CC lentivirus protein R (Vpr) of HIV-1 or -2, or simian immune deficiency
 CC virus, comprising an inhibitor (I) of cellular chaperones (II) that are
 CC essential for proper folding, stability and, thus, biological function of
 CC Vpr. The inhibitor is useful for inhibiting interaction of Vpr with
 CC cyclophilins include cyclosporin A, FK506, rapamycin and the non-
 CC immunosuppressive compounds SDZ NIM811 and/or sangliferin A. Vpr first
 CC binds to cyclophilin A (CypA) to regulate the trans conformation of
 CC proline peptidyl bonds in the N-terminus of Vpr. The inhibitor prevents
 CC cis-trans rearrangement, specifically of pro residues at positions 5, 10,
 CC 14 and 35 of Vpr. The inhibitor may also act by a process in which CypA
 CC co-translationally regulates expression, folding and stability of Vpr and
 CC this stabilizing process is active in cells transfected with the
 CC specified viruses, with DNA that encodes Vpr, or with recombinant Vpr-
 CC encoding retro, adeno, vaccinia or baculo viruses. All essential
 CC functions of Vpr (induction of cell-cycle arrest, apoptosis, increased
 CC viral production and co-activation of glucocorticoid receptors) are
 CC inhibited. The products of the invention have anti-HIV, neurotropic,
 CC nephrotropic and antileptic activity. The inhibitor may be used in
 CC combination with other antiretroviral agents; blockers of reverse
 CC transcription and/or protease; genetically based antiretroviral
 CC therapies, intracellular immunization and administration of anti-HIV gene
 CC in stem cells and/or peripheral CD4+ lymphocytes, especially in advanced
 CC stages of disease. The agent of the invention is used to prevent and
 CC treat lentiviral infections, specifically AIDS or HIV infections
 CC (including where asymptomatic), also HIV-induced dementia (by inhibiting
 CC infection of neurons, glial cells and endothelial cells in cerebral
 CC capillaries), HIV-associated lipodystrophy syndrome or other disorders of
 CC lipid metabolism and HIV-associated nephropathy, also to prevent systemic
 CC infection immediately after exposure to HIV, e.g. needle pricks with HIV-
 CC contaminated blood. This sequence represents the CypA binding fragment at
 CC the N-terminal of the HIV-1(NL4-3) Vpr protein.
 XX
 XX Sequence 96 AA;

Query Match 100.0%; Score 262; DB 7; Length 96;
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWNTLELLELKSEAVRHPRIWLHNLGQHIY 47
 DB 1 MEQAPEDQGPQREPYNEWNTLELLELKSEAVRHPRIWLHNLGQHIY 47

RESULT 11
 ADF46812
 ID ADF46812 standard; protein; 96 AA.
 XX
 AC ADF46812;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE HIV-1 Vpr protein.
 XX
 KW virus protein R; Vpr; functional analysis.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN JP2003259881-A.
 XX
 PD 16-SEP-2003.
 XX
 PF 12-MAR-2002; 2002JP-00066938.
 PR 12-MAR-2002; 2002JP-00066938.
 XX
 PA (ORIY) ORIENTAL YEAST CO LTD.
 XX
 XX (NAKA/) NAKAMURA T.
 DR WPI; 2004-026590/03.
 DR N-PSDB; ADF46813.
 XX

Producing recombinant virus protein R (Vpr), useful in promoting
 immunodeficiency virus reproduction, involves transforming a host cell
 with an expression vector for the protein.
 Claim 1; SEQ ID NO 1; 14pp; Japanese.
 The invention relates to a method of producing a recombinant HIV-1 virus
 protein R (Vpr) protein or a protein having one or more substitutions,
 additions or alterations and having biological activity, by transforming
 a host Escherichia coli cell with an expression vector containing the
 gene encoding Vpr, and culturing the transformed cell. The method is
 useful for producing recombinant Vpr protein. The protein is useful for
 promoting the reproduction of immunodeficiency virus in cell, tissue or
 organ derived from an organism. The protein is useful for functional
 analysis of the Vpr protein. This sequence represents the HIV-1 Vpr
 protein.

Sequence 96 AA;
 Query Match 100.0%; Score 262; DB 8; Length 96;
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWNTLELLELKSEAVRHPRIWLHNLGQHIY 47
 DB 1 MEQAPEDQGPQREPYNEWNTLELLELKSEAVRHPRIWLHNLGQHIY 47

RESULT 12
 ABM79669
 ID ABM79669 standard; protein; 96 AA.
 XX
 AC ABM79669;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE HIV-1 Vpr protein.
 XX
 KW HIV; Vpr; modulator; anti-HIV; virucide.

```

XX OS Human immunodeficiency virus type 1.
XX PN WO2003076621-A2.
XX PD 18-SEP-2003.
XX XX
XX XX 07-MAR-2003; 2003WO-CA000325.
XX PF
XX XX 08-MAR-2002; 2002US-0362384P.
XX PR
XX XX (UIMO-) UNIV MONTREAL.
XX PA
XX PI Cohen EA, Yao X, Belhumeur P, Lemay J;
XX PD WPI; 2004-042337/04.
XX DR
XX XX
XX XX New polypeptides that bind to viral Vpr protein, useful for treatment,
XX PT prevention, diagnosis and prognosis of immune deficiency virus infection.
XX PS
XX XX Example 20; Page 33-34; 143pp; English.
XX XX
XX CC The present invention relates to peptide which are capable of binding to
XX CC the HIV protein vpr and/or modulates vpr-related activity. Such peptides
XX CC are used for prevention, treatment, diagnosis and prognosis of vpr-
XX CC related diseases, particularly lentiviral infection (specifically HIV-1
XX CC or -2, or simian immune deficiency virus), for modulating, particularly
XX CC inhibiting, vpr-related activities and for detecting vpr in a sample.
XX CC Nucleic acids encoding such peptides and cells that contain this nucleic
XX CC acid can also be used therapeutically. The present sequence is a protein
XX CC of relevance to the invention
XX CC
XX SQ Sequence 96 AA;

Query Match 100.0%; Score 262; DB 8; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.6e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGQRPYNEWTLEELKSEAVRHPRIWLHNLGQHIY 47
DB 1 MEQAPEDQGQRPYNEWTLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 13
ABR55491
ID ABR55491 standard; protein; 96 AA.
XX AC
XX AC ABR55491;
XX DT
XX DT 11-AUG-2003 (first entry)
XX DE
XX DE Amino acid sequence of a HIV vpr protein.
XX KW
XX KW Polymorphic marker; host response; HIV; AIDS related virus; vaccine;
XX KW hepatitis related virus; HCV; HBV; drug resistance; vpr.
XX OS
XX OS Human immunodeficiency virus.
XX PN
XX PN WO2003035097-A1.
XX PD
XX PD 01-MAY-2003.
XX XX
XX XX 23-OCT-2002; 2002WO-AU001450.
XX PF
XX PF
XX XX 23-OCT-2001; 2001AU-00008425.
XX PR
XX PR (EPIP-) EPIPOT PTY LTD.
XX PA
XX PA Mallal S;
XX PI
XX PI
XX DR
XX DR WPI; 2003-449231/42.
XX PT

Determining the influence of variation in host genes on the selection of

PT microorganisms with protein substitutions, comprises typing individuals
PT of a cohort infected with a microorganism for an intrinsic polymorphic
PT marker.
XX PS Claim 22; Page 89; 157pp; English.
XX XX
XX CC The specification describes a method of determining the influence of
XX CC variation in host genes on selection of microorganisms with protein
XX CC substitutions. The method comprises typing all individuals of a
XX CC population of patients infected with a microorganism for at least one
XX CC selected intrinsic polymorphic marker involved in the host response to
XX CC the presence of the microorganism. The method is useful for examining
XX CC selective pressures confronting a wide range of organisms that exhibit
XX CC pathogenic traits in a host, such as bacteria, fungi, mycobacterium,
XX CC viruses and virus-like particles; for examining microorganisms that have
XX CC adapted to evolve rapidly, including HIV and AIDS related viruses and the
XX CC hepatitis related viruses such as HCV and HBV. The method is useful for
XX CC designing a vaccine to prevent or delay the emergence of drug resistance
XX CC in patients treated with a particular drug specific for a microorganism
XX CC where the drug affects the replication of the microorganism at the
XX CC nucleotide or amino acid level. The present sequence represents a HIV vpr
XX CC protein, which is expected to provide optimal cytotoxic T lymphocyte
XX CC (CTL) induced therapeutic protection to the cohort examined in that study
XX SQ Sequence 96 AA;

Query Match 97.7%; Score 256; DB 6; Length 96;
Best Local Similarity 97.9%; Pred. No. 3.9e-25;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGQRPYNEWTLEELKSEAVRHPRIWLHNLGQHIY 47
DB 1 MEQAPEDQGQRPYNEWTLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 14
AAB69306
ID AAB69306 standard; protein; 96 AA.
XX AC
XX AC AAB69306;
XX DT
XX DT 12-SEP-2003 (revised)
XX DT 20-APR-2001 (first entry)
XX DE
XX DE HIV-1 non-subtype B clone 93BR029-4 vpr protein.
XX KW
XX KW HIV-1; human immunodeficiency virus; non-subtype B; gag; pol; env; vpu;
XX KW vif; vpr; tat; rev; nef; vaccine.
XX OS
XX OS Human immunodeficiency virus 1.
XX PN
XX PN WO200026416-A1.
XX PD
XX PD 11-MAY-2000.
XX XX
XX XX 25-OCT-1999; 99WO-US024837.
XX PF
XX PF
XX XX 02-NOV-1998; 98US-00184418.
XX PR
XX PR (UABR-) UAB RES FOUND.
XX PA
XX PA Hahn BH, Shaw GM, Gao F;
XX PI
XX PI
XX DR
XX DR WPI; 2000-365651/31.
XX XX
XX XX Novel genomic nucleic acids of non-subtype B human immunodeficiency virus
XX PT type 1 useful for detecting and treating AIDS comprises a specific
XX PT nucleotide sequence.
XX PS
XX PS Claim 41; Fig 17; 131pp; English.
XX XX
XX CC The present invention provides the protein and coding sequences for a
XX CC number of human immunodeficiency virus (HIV) type 1 non-subtype B

```

CC isolates. The sequences shown include the near full-length coding
 CC sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat,
 CC rev and nef proteins. These can be used to detect the presence of HIV-1
 CC in a sample and to produce antibodies against non-subtype B HIV-1 virus.
 CC These antibodies can be used in vaccines to prevent and treat HIV
 CC infection. (Updated on 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 96 AA;

Query Match 97.3%; Score 255; DB 3; Length 96;
 Best Local Similarity 95.7%; Pred. NO. 5.3e-25;
 Matches 45; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHFPRWLHNLGQHIY 47
 |||||
 DB 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHFPRWLHNLGQHIY 47

RESULT 15

AAU80187
 ID AAU80187 standard; protein; 96 AA.

XX
 AC AAU80187;

DT 29-AUG-2003 (revised)

DI 15-JUL-2002 (first entry)

XX
 DE HIV-1 Vpr protein.

XX HIV-1; acquired immunodeficiency syndrome; AIDS; Vpr.

XX Human immunodeficiency virus 1.

XX Key Location/Qualifiers

FT Misc-difference 45
 FT /note= "Encoded by CAT"

XX JP2002085099-A.

XX 26-MAR-2002.

XX 14-SEP-2000; 2000JP-00280851.

XX 14-SEP-2000; 2000JP-00280851.

XX (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.

XX (ORIY) ORIENTAL YEAST CO LTD.

XX WPI; 2002-378279/41.

XX N-PSDB; ABK50386.

XX Detection of immunodeficiency virus by detecting the presence of Vpr
 protein.

XX Disclosure; Page 8; 17pp; Japanese.

XX The invention relates to a method for detecting immunodeficiency virus in
 CC a sample in which the presence of Vpr (not defined) protein in the sample
 CC is detected. Also included are a kit for use in the above detecting
 CC method containing a cell and a pigment, and a method for screening a
 CC compound promoting or inhibiting the intake of a substance having a
 CC molecular weight (M.W.) of 300 to 3000 in which the promotion or the
 CC inhibition of intake of the substance by the presence of a test compound
 CC is used as the index in the intake of the substance to the cell by a
 CC treatment using a sample containing Vpr protein. The method is used for
 CC detecting immunodeficiency virus (e.g. Human immunodeficiency virus-1,
 CC the causative agent of acquired immunodeficiency virus syndrome, AIDS) in
 CC a sample. The present sequence represents HIV-1 Vpr. (Updated on 29-AUG-
 CC 2003 to standardise OS field)

XX Sequence 96 AA;

Query Match 96.2%; Score 252; DB 5; Length 96;

Best Local Similarity 97.9%; Pred. NO. 1.3e-24;
 Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHFPRWLHNLGQHIY 47
 |||||
 DB 1 MEQAPEDQGPQREPYNWTLLEELKSEAVRHFPRWLHNLGQHIY 47

Search completed: October 18, 2004, 18:45:32
 Job time : 63.6875 secs

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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:42:45 ; Search time 27.4167 Seconds
(without alignments)
113.688 Million cell updates/sec

Title: US-09-913-927D-2
Perfect score: 262
Sequence: 1 MEQAPEDQGPQREPYNEWTL.....SEAVRHPRFWLHNLGQHIY 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 262 | 100.0 | 96 | 4 | US-09-309-572-19 |
| 2 | 262 | 100.0 | 96 | 4 | US-09-718-096-19 |
| 3 | 252 | 96.2 | 96 | 3 | US-08-704-856C-15 |
| 4 | 252 | 96.2 | 96 | 4 | US-09-242-881-15 |
| 5 | 249 | 95.0 | 96 | 4 | US-09-839-329-1 |
| 6 | 248 | 94.7 | 72 | 2 | US-08-301-915-4 |
| 7 | 248 | 94.7 | 72 | 3 | US-08-524-694A-4 |
| 8 | 248 | 94.7 | 72 | 4 | US-09-454-156A-4 |
| 9 | 248 | 94.7 | 78 | 3 | US-09-124-900-5 |
| 10 | 248 | 94.7 | 96 | 2 | US-08-301-915-1 |
| 11 | 248 | 94.7 | 96 | 3 | US-08-524-694A-1 |
| 12 | 248 | 94.7 | 96 | 4 | US-09-454-156A-1 |
| 13 | 238 | 90.8 | 95 | 4 | US-09-319-588C-10 |
| 14 | 220 | 84.0 | 100 | 4 | US-09-462-917A-116 |
| 15 | 209 | 79.8 | 100 | 4 | US-09-462-917A-115 |
| 16 | 206 | 78.6 | 93 | 4 | US-09-462-917A-117 |
| 17 | 194 | 74.0 | 100 | 4 | US-09-462-917A-118 |
| 18 | 138 | 52.7 | 100 | 4 | US-09-206-551-49 |
| 19 | 118 | 45.0 | 3077 | 6 | 5223423-2 |
| 20 | 111 | 42.4 | 105 | 2 | US-08-301-915-2 |
| 21 | 111 | 42.4 | 105 | 3 | US-08-524-694A-2 |
| 22 | 111 | 42.4 | 105 | 4 | US-09-454-156A-2 |
| 23 | 110 | 42.0 | 20 | 3 | US-09-055-075C-8 |
| 24 | 110 | 42.0 | 20 | 4 | US-09-919-124-8 |
| 25 | 110 | 42.0 | 21 | 5 | PCT-US94-02191-4 |
| 26 | 103 | 39.3 | 105 | 2 | US-08-659-251-9 |
| 27 | 103 | 39.3 | 105 | 3 | US-09-256-490-9 |

Sequence 9, Appli
Sequence 10, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 33, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 5, Appl
Sequence 8, Appl
Sequence 36, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 60286, A
Sequence 44816, A
Sequence 3, Appli
Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-309-572-19
; Sequence 19, Application US/09309572
; Patent No. 6440730
; GENERAL INFORMATION:
; APPLICANT: Heinrich-Pette-Institut
; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
; FILE REFERENCE: P50489
; CURRENT APPLICATION NUMBER: US/09/309,572
; CURRENT FILING DATE: 1999-05-11
; EARLIER APPLICATION NUMBER: DE 198 56 463
; EARLIER FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: vpr protein
US-09-309-572-19

Query Match 100.0%; Score 262; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.8e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPRFWLHNLGQHIY 47
|||||
DB 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPRFWLHNLGQHIY 47

RESULT 2
US-09-718-096-19
; Sequence 19, Application US/09718096
; Patent No. 6585763
; GENERAL INFORMATION:
; APPLICANT: Von Laer, Meike-Dorothee
; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
; FILE REFERENCE: 35-195
; CURRENT APPLICATION NUMBER: US/09/718,096
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: DE 19856463.5
; PRIOR FILING DATE: 1998-11-26
; PRIOR APPLICATION NUMBER: EP 99250415.9
; PRIOR FILING DATE: 1999-11-25
; PRIOR APPLICATION NUMBER: US 09/309,572
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19

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; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: vpr protein
US-09-718-096-19

Query Match      100.0%; Score 262; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.8e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47
   |||||
Db 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 3
US-08-704-856C-15
; Sequence 15, Application US/08704856C
; Patent No. 6042832
; GENERAL INFORMATION:
; APPLICANT: Koprowski, Hilary
; APPLICANT: Yusibov, Vidadi
; APPLICANT: Hooper, Douglas, C.
; APPLICANT: Modelska, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/242,881
; FILING DATE: 25-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,856
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-242-881-15

Query Match      96.2%; Score 252; DB 4; Length 96;
Best Local Similarity 95.7%; Pred. No. 3.9e-26;
Matches 45; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47
   |||||
Db 1 MEQAPEDQGQPREPYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 5
US-09-839-329-1
; Sequence 1, Application US/09839329
; Patent No. 6664040
; GENERAL INFORMATION:
; APPLICANT: Michael P. Sherman
; APPLICANT: Warner C. Greene
; APPLICANT: Carlos M.C. de No. 6664040ohna
; APPLICANT: Ulrich Schubert
; APPLICANT: Peter Henklein
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
; FILE REFERENCE: G&C 30448.91-US-U2
; CURRENT APPLICATION NUMBER: US/09/839,329
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/206,610
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/267,827
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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;; COUNTRY: U.S.A.
;; ZIP: 07601
;; COMPUTER READABLE FORM: disk
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/454,156A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/301,915
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: JACKSON, David A.
;; REGISTRATION NUMBER: 26,742
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-487-5800
;; TELEFAX: 201-343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 72 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
US-09-454-156A-4

Query Match 94.7%; Score 248; DB 4; Length 72;
Best Local Similarity 93.6%; Pred. No. 9.3e-26;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNWNTLELLELKSEAVRHPRIWLHNLGQHIY 47
DB 1 MEQAPEDQGPQREPNWNTLELLELKSEAVRHPRIWLHNLGQHIY 47

RESULT 9
US-09-124-900-5
; Sequence 5, Application US/09124900
; Patent No. 6268484
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; APPLICANT: BUCHACHER, Andrea
; APPLICANT: ERNST, Wolfgang
; APPLICANT: BALLAUN, Claudia
; APPLICANT: PURTSCHER, Martin
; APPLICANT: TRKOLA, Alexandra
; APPLICANT: FREDL, Renate
; APPLICANT: SCHMATZ, Christine
; APPLICANT: KLIMA, Annelies
; APPLICANT: STEINDL, Franz
; APPLICANT: MUSTER, Thomas
; TITLE OF INVENTION: HIV-Vaccines
; FILE REFERENCE: 1939-112P
; CURRENT APPLICATION NUMBER: US/09/124,900
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/BP95/01481
; PRIOR FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 5
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-124-900-5

Query Match 94.7%; Score 248; DB 3; Length 78;
Best Local Similarity 93.6%; Pred. No. 1e-25;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNWNTLELLELKSEAVRHPRIWLHNLGQHIY 47
DB 1 MEQAPEDQGPQREPNWNTLELLELKSEAVRHPRIWLHNLGQHIY 47

RESULT 10
US-08-301-915-1
; Sequence 1, Application US/08301915
; Patent No. 5861161
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,915
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-301-915-1

Query Match 94.7%; Score 248; DB 2; Length 96;
Best Local Similarity 93.6%; Pred. No. 1.3e-25;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNWNTLELLELKSEAVRHPRIWLHNLGQHIY 47
DB 1 MEQAPEDQGPQREPNWNTLELLELKSEAVRHPRIWLHNLGQHIY 47

RESULT 11
US-08-524-694A-1
; Sequence 1, Application US/08524694A
; Patent No. 6043081
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED
; TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES

; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,694A
; FILING DATE: September 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-524-694A-1

Query Match 94.7%; Score 248; DB 3; Length 96;
Best Local Similarity 93.6%; Pred. No. 1.3e-25;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MEQAPEDQGQRPYPNWTLEELKSEAVRHPRIWLHNLGHQIY 47
Db 1 MEQAPEDQGQRPYPNWTLEELKSEAVRHPRIWLHNLGHQIY 47

RESULT 12
US-09-454-156A-1
; Sequence 1, Application US/09454156A
; Patent No. 6468539
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454,156A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/301,915
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-454-156A-1

Query Match 94.7%; Score 248; DB 4; Length 96;
Best Local Similarity 93.6%; Pred. No. 1.3e-25;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MEQAPEDQGQRPYPNWTLEELKSEAVRHPRIWLHNLGHQIY 47
Db 1 MEQAPEDQGQRPYPNWTLEELKSEAVRHPRIWLHNLGHQIY 47

RESULT 13
US-09-319-588C-10
; Sequence 10, Application US/09319588C
; Patent No. 6509018
; GENERAL INFORMATION:
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INSERM
; APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS
; APPLICANT: INSTITUT PASTEUR
; APPLICANT: MAUCLERE, Philippe
; APPLICANT: LOUSSERT-AJAKA, Ibtissam
; APPLICANT: SIMON, Francois
; APPLICANT: SARAGOSTI, Sentob
; APPLICANT: BARRE-SINOUSI, Francoise
; TITLE OF INVENTION: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATIONS.
; FILE REFERENCE: 598US12
; CURRENT APPLICATION NUMBER: US/09/319,588C
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: FR96/15087
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-319-588C-10

Query Match 90.8%; Score 238; DB 4; Length 95;
Best Local Similarity 89.4%; Pred. No. 2.8e-24;
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MEQAPEDQGQRPYPNWTLEELKSEAVRHPRIWLHNLGHQIY 47
Db 1 MERAPDAGFQRPYPNWTLEELKSEAVRHPRIWLHNLGHQIY 47

RESULT 14
US-09-462-917A-116
; Sequence 116, Application US/09462917A
; Patent No. 6511801
; GENERAL INFORMATION:
; APPLICANT: Delaporte, Eric
; APPLICANT: Peeters, Martine
; APPLICANT: Saman, Eric
; APPLICANT: Vanden Haesevelde, Marlen

```
; TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof
; FILE REFERENCE: INNS:014 11362.0014.NPUS00
; CURRENT APPLICATION NUMBER: US/09/462,917A
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: PCT/EP98/04522
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Human
US-09-462-917A-116
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Query Match 84.0%; Score 220; DB 4; Length 100;
Best Local Similarity 85.1%; Pred. No. 7.4e-22;
Matches 40; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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QY 1 MEQAPEDQGPQREPNYNTWLELLELKSEAVRHPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGPAREPNFNTWLELLELKSEAVRHPRIWLHNLGQHIY 47
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RESULT 15

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US-09-462-917A-115
; Sequence 115, Application US/09462917A
; Patent No. 6511801
; GENERAL INFORMATION:
; APPLICANT: Delaporte, Eric
; APPLICANT: Peeters, Martine
; APPLICANT: Saman, Eric
; APPLICANT: Vanden Haesevelde, Marlen
; TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof
; FILE REFERENCE: INNS:014 11362.0014.NPUS00
; CURRENT APPLICATION NUMBER: US/09/462,917A
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: PCT/EP98/04522
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Human
US-09-462-917A-115
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Query Match 79.8%; Score 209; DB 4; Length 100;
Best Local Similarity 78.7%; Pred. No. 2.2e-20;
Matches 37; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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QY 1 MEQAPEDQGPQREPNYNTWLELLELKSEAVRHPRIWLHNLGQHIY 47
Db 1 MERAPEDQGPAREPNFNTWLELLELKSEAVRHPRIWLHNLGQHIY 47
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Search completed: October 18, 2004, 18:49:22
Job time : 28.4167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2004, 18:43:30 ; Search time 85.1875 Seconds
(without alignments)
178.383 Million cell updates/sec

Title: US-09-913-927D-2

Perfect score: 262

Sequence: 1 MEQAPEDQGPQREPNYEWTL.....SEAVRHFPRIWLHNLGQHIY 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pap.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pap.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pap.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pap.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pap.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pap.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 262 | 100.0 | 96 | 14 | US-10-059-261-272 |
| 2 | 249 | 95.0 | 96 | 9 | US-09-839-329-1 |
| 3 | 248 | 94.7 | 78 | 14 | US-10-283-618-15 |
| 4 | 248 | 94.7 | 96 | 14 | US-10-190-435-284 |
| 5 | 244 | 93.1 | 96 | 14 | US-10-190-435-276 |
| 6 | 240 | 91.6 | 96 | 14 | US-10-190-435-264 |
| 7 | 240 | 91.6 | 96 | 14 | US-10-190-435-265 |
| 8 | 240 | 91.6 | 96 | 14 | US-10-190-435-266 |
| 9 | 240 | 91.6 | 96 | 14 | US-10-190-435-282 |
| 10 | 240 | 91.6 | 96 | 14 | US-10-190-435-283 |
| 11 | 240 | 91.6 | 96 | 15 | US-10-296-734-4 |
| 12 | 240 | 91.6 | 96 | 15 | US-10-296-734-1475 |
| 13 | 239 | 91.2 | 96 | 14 | US-10-190-435-258 |
| 14 | 239 | 91.2 | 96 | 14 | US-10-190-435-259 |

| | | | | | | |
|----|-----|------|-----|----|--------------------|-------------------|
| 15 | 239 | 91.2 | 96 | 14 | US-10-190-435-273 | Sequence 273, App |
| 16 | 238 | 90.8 | 95 | 14 | US-10-301-661A-10 | Sequence 10, Appl |
| 17 | 238 | 90.8 | 96 | 14 | US-10-190-435-262 | Sequence 262, App |
| 18 | 237 | 90.5 | 96 | 14 | US-10-190-435-254 | Sequence 254, App |
| 19 | 237 | 90.5 | 96 | 14 | US-10-190-435-285 | Sequence 285, App |
| 20 | 237 | 90.5 | 96 | 14 | US-10-190-435-278 | Sequence 278, App |
| 21 | 236 | 90.1 | 96 | 14 | US-10-190-435-263 | Sequence 263, App |
| 22 | 235 | 89.7 | 96 | 14 | US-10-190-435-256 | Sequence 256, App |
| 23 | 235 | 89.7 | 96 | 14 | US-10-190-435-257 | Sequence 257, App |
| 24 | 234 | 89.3 | 96 | 14 | US-10-469-199-2 | Sequence 2, Appli |
| 25 | 234 | 89.3 | 362 | 15 | US-10-190-435-260 | Sequence 260, App |
| 26 | 233 | 88.9 | 96 | 14 | US-10-190-435-261 | Sequence 261, App |
| 27 | 233 | 88.9 | 96 | 14 | US-10-190-435-274 | Sequence 274, App |
| 28 | 233 | 88.9 | 96 | 14 | US-10-190-435-277 | Sequence 277, App |
| 29 | 233 | 88.9 | 96 | 16 | US-10-325-468-36 | Sequence 36, Appl |
| 30 | 233 | 88.9 | 96 | 14 | US-10-190-435-268 | Sequence 268, App |
| 31 | 232 | 88.5 | 96 | 14 | US-10-190-435-269 | Sequence 269, App |
| 32 | 232 | 88.5 | 96 | 14 | US-10-190-435-279 | Sequence 279, App |
| 33 | 230 | 87.8 | 96 | 14 | US-10-325-468-11 | Sequence 11, Appl |
| 34 | 229 | 87.4 | 96 | 16 | US-10-190-435-267 | Sequence 267, App |
| 35 | 227 | 86.6 | 96 | 14 | US-10-296-734-1477 | Sequence 1477, Ap |
| 36 | 226 | 86.3 | 94 | 15 | US-10-190-435-270 | Sequence 270, App |
| 37 | 225 | 85.9 | 96 | 14 | US-10-190-435-271 | Sequence 271, App |
| 38 | 225 | 85.9 | 96 | 14 | US-10-190-435-280 | Sequence 280, App |
| 39 | 222 | 84.7 | 96 | 14 | US-09-971-980-63 | Sequence 63, Appl |
| 40 | 222 | 84.0 | 68 | 9 | US-10-320-786-116 | Sequence 116, App |
| 41 | 220 | 84.0 | 100 | 14 | US-10-190-435-281 | Sequence 281, App |
| 42 | 220 | 84.0 | 96 | 14 | US-10-190-435-272 | Sequence 272, App |
| 43 | 219 | 83.6 | 96 | 14 | US-10-320-786-115 | Sequence 115, App |
| 44 | 216 | 82.4 | 96 | 14 | | |
| 45 | 209 | 79.8 | 100 | 14 | | |

ALIGNMENTS

RESULT 1

US-10-059-261-272
; Sequence 272, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC TRANSITION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: FUNCTION OF THE PTPC
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 272
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-059-261-272

Query Match 100.0%; Score 262; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPNYEWTLLEELKSEAVRHFPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGPQREPNYEWTLLEELKSEAVRHFPRIWLHNLGQHIY 47

RESULT 2

US-09-839-329-1
; Sequence 1, Application US/09839329

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; Publication No. US20020022027A1
; GENERAL INFORMATION:
; APPLICANT: Michael P. Sherman
; APPLICANT: Warner C. Greene
; APPLICANT: Carlos M.C. de No. 6664040ohna
; APPLICANT: Ulrich Schubert
; APPLICANT: Peter Henklein
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
; FILE REFERENCE: G&C 30448-91-US-02
; CURRENT APPLICATION NUMBER: US/09/839,329
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/206,610
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/267,827
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide of regulatory virus proteins R
; OTHER INFORMATION: (vpr) of human immunodeficiency virus type 1
; OTHER INFORMATION: (HIV-1)
US-09-839-329-1

Query Match          95.0%; Score 249; DB 9; Length 96;
Best Local Similarity 97.9%; Pred. No. 8.2e-23;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGPQREPNYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 3
US-10-283-618-15
; Sequence 15, Application US/10283618
; Publication No. US20030165517A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; APPLICANT: Walker, Bruce
; TITLE OF INVENTION: THERAPEUTIC ANTI-HIV (vpr) COMPOUNDS
; FILE REFERENCE: G2 2111.00
; CURRENT APPLICATION NUMBER: US/10/283,618
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/345,957
; PRIOR FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-10-283-618-15

Query Match          94.7%; Score 248; DB 14; Length 78;
Best Local Similarity 93.6%; Pred. No. 8.6e-23;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGPQREPNYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 4
US-10-190-435-284
; Sequence 284, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
US-10-190-435-284
```

```
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr HXB2
US-10-190-435-284

Query Match          94.7%; Score 248; DB 14; Length 96;
Best Local Similarity 93.6%; Pred. No. 1.1e-22;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGPQREPNYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 5
US-10-190-435-276
; Sequence 276, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 276
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr 92BR025
US-10-190-435-276

Query Match          93.1%; Score 244; DB 14; Length 96;
Best Local Similarity 93.6%; Pred. No. 3.4e-22;
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPNYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGPQREPNYNEWTLLEELKSEAVRHPRIWLHNLGQHIY 47

RESULT 6
US-10-190-435-264
; Sequence 264, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
```



```

/ GENERAL INFORMATION:
/ APPLICANT: ZUR MEGEDE, Jan
/ APPLICANT: BARNETT, Susan W.
/ APPLICANT: LIAN, Ying
/ APPLICANT: ENGELBRECHT, Susan
/ APPLICANT: VAN RENSBURG, Esrelita J.
/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
/ TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
/ FILE REFERENCE: PP18133.003 / 2302-18133
/ CURRENT APPLICATION NUMBER: US/10/190,435
/ CURRENT FILING DATE: 2002-12-30
/ NUMBER OF SEQ ID NOS: 319
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 283
/ LENGTH: 96
/ TYPE: PRT
/ ORGANISM: Artificial Sequence

```

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr C2220-Eth
US-10-190-435-283

Query Match          91.6%; Score 240; DB 14; Length 96;
Best Local Similarity 91.5%; Pred. No. 1e-21;
Matches 43; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47

RESULT 11
US-10-296-734-4
; Sequence 4, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VPR consensus polypeptide
US-10-296-734-4

Query Match          91.6%; Score 240; DB 15; Length 96;
Best Local Similarity 91.5%; Pred. No. 1e-21;
Matches 43; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47

RESULT 12
US-10-296-734-1475
; Sequence 1475, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1475
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-296-734-1475

Query Match          91.6%; Score 240; DB 15; Length 96;
Best Local Similarity 91.5%; Pred. No. 1e-21;
Matches 43; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
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RESULT 13
US-10-190-435-258
; Sequence 258, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 258
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV008-17
US-10-190-435-258

Query Match          91.2%; Score 239; DB 14; Length 96;
Best Local Similarity 89.4%; Pred. No. 1.4e-21;
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47

RESULT 14
US-10-190-435-259
; Sequence 259, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 259
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV008-1
US-10-190-435-259

Query Match          91.2%; Score 239; DB 14; Length 96;
Best Local Similarity 89.4%; Pred. No. 1.4e-21;
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47
Db 1 MEQAPDQGPQREPYNEWTLLEELKSEAVRHPRIWLNHNGQIY 47

RESULT 15
US-10-190-435-273
; Sequence 273, Application US/10190435
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; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 273
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV012-4
US-10-190-435-273

Query Match          91.2%; Score 239; DB 14; Length 96;
Best Local Similarity 89.4%; Fred. No. 1.4e-21;
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 MEQAPDQGPQREPYNWTLLEELKSEAVRHPRIWLHNLGQHIY 47
|||||
DB      1 MEQAPDQGPQREPYNWALELLEELKQEA VRHPRPWLHSLGQHIY 47
|||||
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Search completed: October 18, 2004, 18:52:22
Job time : 85.1875 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:38:31 ; Search time 16.6458 Seconds
(without alignments)
271.671 Million cell updates/sec

Title: US-09-913-927D-2

Perfect score: 262

Sequence: 1 MEQAPDQGPQRPYNEWTLLLEELKSEAVRHFPRIWLHNLGQHIY 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|------------------------|
| 1 | 251 | 95.8 | 96 | 2 S54380 | vpr protein - huma |
| 2 | 247 | 94.3 | 95 | 2 T09383 | vpr protein - huma |
| 3 | 247 | 94.3 | 96 | 2 T09444 | vpr protein - huma |
| 4 | 242 | 92.4 | 96 | 2 T01670 | vpr protein - huma |
| 5 | 239 | 91.2 | 97 | 1 D44001 | vpr protein - huma |
| 6 | 215 | 82.1 | 96 | 1 ASLJSC | vpr protein - simi |
| 7 | 154 | 58.8 | 97 | 2 S03067 | gene R protein - h |
| 8 | 148 | 56.5 | 101 | 1 ASLJR3 | vpr protein - simi |
| 9 | 147.5 | 56.3 | 122 | 1 ASLJRS | vpr protein - simi |
| 10 | 145 | 55.3 | 89 | 2 S07991 | vpr protein - simi |
| 11 | 143 | 54.6 | 101 | 2 T11563 | vpr protein - simi |
| 12 | 134 | 51.1 | 104 | 2 S28083 | vpr protein - simi |
| 13 | 128 | 48.9 | 105 | 2 S53095 | vpr protein - huma |
| 14 | 125 | 47.7 | 101 | 2 S08439 | vpr protein - huma |
| 15 | 121 | 46.2 | 104 | 1 ASLJCY | vpr protein - huma |
| 16 | 112.5 | 42.9 | 104 | 1 ASLJSY | vpr protein - huma |
| 17 | 111 | 42.4 | 105 | 1 ASLJR2 | vpr protein - huma |
| 18 | 103 | 39.3 | 105 | 2 S12156 | vpr protein - huma |
| 19 | 94 | 35.9 | 105 | 1 ASLJGR | vpr protein - huma |
| 20 | 87 | 33.2 | 140 | 2 S46351 | vpx protein - simi |
| 21 | 76.5 | 29.2 | 311 | 2 A10275 | DNA replication te |
| 22 | 67.5 | 25.8 | 119 | 1 ASLJX4 | vpu protein - simi |
| 23 | 64 | 24.4 | 508 | 1 P1WL | L1 protein - huma |
| 24 | 63.5 | 24.2 | 154 | 2 S36993 | transposase (clone |
| 25 | 61 | 23.3 | 392 | 1 FOLJGA | gag polyprotein - |
| 26 | 61 | 23.3 | 392 | 1 FOLJGB | gag polyprotein - |
| 27 | 61 | 23.3 | 392 | 1 FOLJSE | gag polyprotein - bovi |
| 28 | 60.5 | 23.1 | 308 | 2 B60672 | blastula butanol-e |
| 29 | 60.5 | 23.1 | 865 | 2 B64618 | preprotein translo |

| | | | | | |
|----|------|------|------|----------|--------------------|
| 30 | 60 | 22.9 | 294 | 2 A60672 | blastula butanol-e |
| 31 | 59.5 | 22.7 | 3165 | 2 S15010 | hypothetical prote |
| 32 | 59 | 22.5 | 298 | 2 B64180 | araC-like transcri |
| 33 | 59 | 22.5 | 1206 | 2 D84542 | probable chloropla |
| 34 | 58 | 22.1 | 327 | 2 AH2608 | transcription regu |
| 35 | 58 | 22.1 | 327 | 2 G97390 | arac family transc |
| 36 | 58 | 22.1 | 384 | 2 D65103 | agac protein - Esc |
| 37 | 58 | 22.1 | 384 | 2 H91130 | hypothetical prote |
| 38 | 58 | 22.1 | 384 | 2 H85975 | hypothetical prote |
| 39 | 58 | 22.1 | 797 | 2 A71267 | hypothetical prote |
| 40 | 57.5 | 21.9 | 106 | 2 A30996 | orf-X protein - si |
| 41 | 57.5 | 21.9 | 112 | 1 ASLJX3 | vpu protein - simi |
| 42 | 57.5 | 21.9 | 112 | 1 ASLJST | vpu protein - simi |
| 43 | 57.5 | 21.9 | 112 | 2 S03066 | gene X protein - h |
| 44 | 57.5 | 21.9 | 148 | 2 D75205 | molybdopterin bios |
| 45 | 57.5 | 21.9 | 149 | 2 F71240 | molybdopterin bios |

ALIGNMENTS

RESULT 1

S54380

vpr protein - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S54380

R;Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A;Reference number: S54377

A;Accession: S54380

A;Status: preliminary

A;Molecule type: Genomic RNA

A;Residues: 1-96 <THE>

A;Cross-references: UNIPROT:P12519; EMBL:M22639; MID:g329377; PIDN:AAA45368.1; PID:g329377

C;Superfamily: AIDS vpr protein

Query Match 95.8%; Score 251; DB 2; Length 96;
Best Local Similarity 95.7%; Pred. No. 1.5e-23;
Matches 45; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPDQGPQRPYNEWTLLLEELKSEAVRHFPRIWLHNLGQHIY 47

Db 1 MEQAPDQGPQRPYNEWTLLLEELKSEAVRHFPRIWLHNLGQHIY 47

RESULT 2

T09383

vpr protein - human immunodeficiency virus type 1 (isolate cntrl 1)

C;Species: human immunodeficiency virus type 1, HIV-1

A;Variety: isolate cntrl 1

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T09383

R;Michael, N.B.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Buech, M.P.; Birs

J. Virol. 69, 4228-4236, 1995

A;Title: Defective accessory genes in a human immunodeficiency virus type 1-infected long

A;Reference number: Z16654; MID:95287475; PMID:7769682

A;Accession: T09383

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-95 <MTC>

A;Cross-references: UNIPROT:Q71925; EMBL:U24451; MID:g829440; PIDN:AAA79575.1; PID:g8294

A;Gene: vpr

C;Superfamily: AIDS vpr protein

C;Keywords: AIDS; immunodeficiency

Query Match 94.3%; Score 247; DB 2; Length 95;

Best Local Similarity 91.5%; Pred. No. 4.7e-23;

Matches 43; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEQAPDQGPQRPYNEWTLLLEELKSEAVRHFPRIWLHNLGQHIY 47

Db 1 MEQAPDQGPQRPYNEWTLLLEELKSEAVRHFPRIWLHNLGQHIY 47


```
C;Genetics:
A;Gene: vpr
C;Superfamily: AIDS vpr protein

Query Match      55.3%; Score 145; DB 2; Length 89;
Best Local Similarity 59.6%; Pred. No. 1.1e-10;
Matches 28; Conservative 10; Mismatches 7; Indels 2; Gaps 2;

Qy 2 EQAPEDGQPREPYNEWNTLELLELKSEAVRHF-PRIVLHNLGHYIY 47
   |:|::|||::|||:|::|||::|||::|||::|||::|||::|||::|||
Db 3 ERPEDEAPQREPWDEWVVEELKEALKHFDPRLL-LTALGNVIY 48

RESULT 11
Tl1563
vpr protein - simian immunodeficiency virus SIVsm (strain E543)
C;Species: simian immunodeficiency virus SIVsm
A;Variety: strain E543
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: Tl1563
R;Hirsch, V.M.; Adger-Johnson, D.; Cambell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.; et al.
J. Virol. 71, 1608-1620, 1997
A;Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodeficient
A;Reference number: Z1785; MUID:97151152; PMID:8995688
A;Accession: Tl1563
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-101 <HIR>
A;Cross-references: UNIPROT:P89157; EMBL:U72748; NID:g1695908; PIDN:AAC56562.1; PID:g1695909;
C;Genetics:
A;Gene: vpr
C;Superfamily: AIDS vpr protein
C;Keywords: AIDS; immunodeficiency

Query Match      54.6%; Score 143; DB 2; Length 101;
Best Local Similarity 57.4%; Pred. No. 2.3e-10;
Matches 27; Conservative 11; Mismatches 7; Indels 2; Gaps 2;

Qy 2 EQAPEDGQPREPYNEWNTLELLELKSEAVRHF-PRIVLHNLGHYIY 47
   |:|::|||::|||:|::|||::|||::|||::|||::|||::|||::|||
Db 3 ERPEDEAPQREPWDEWVVEELKEALKHFDPRLL-LTALGNVIY 48

RESULT 12
S28083
vpr protein - simian immunodeficiency virus
C;Species: simian immunodeficiency virus, SIV
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Accession: S28083
R;Tajima, H.; Hasegawa, A.; Makino, N.; Fukasawa, M.; Miura, T.; Speidel, S.; Cooper, R.
Nature 341, 539-541, 1999
A;Title: Sequence of a novel simian immunodeficiency virus from a wild-caught African mar
A;Reference number: S28080; MUID:90015168; PMID:2797181
A;Accession: S28083
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-104 <TSU>
A;Cross-references: GB:M27470; EMBL:X15781; NID:g334683; PIDN:AAB49571.1; PID:g334689
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1989
C;Genetics:
A;Gene: vpr
C;Superfamily: AIDS vpr protein

Query Match      51.1%; Score 134; DB 2; Length 104;
Best Local Similarity 52.3%; Pred. No. 3e-09;
Matches 23; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 2 EQAPEDGQPREPYNEWNTLELLELKSEAVRHF-PRIVLHNLGHYIY 45
   |:|::|||::|||:|::|||::|||::|||::|||::|||::|||::|||
Db 7 EQVSEDGQPREPNQLADTMEEIKKARKHFPPLIILNAVSEY 50

RESULT 13
```

Search completed: October 18, 2004, 18:48:20
Job time : 17.6458 secs

2 EQAPEDQGPQRPEYNWTELLLELKSEAVRHFPRIWLNLGHHY 47
+ ||||| : : : : :
7 ELPEDGTPPREPGDWFVIELREITEALKHFDRLSLTALGHIIY 52

C;Superfamily: AIDS vpr protein

| | | | | | | | | | |
|---------|-----|--------------|----|------------|-----|--------|----|------|----|
| Matches | 26; | Conservative | 8; | Mismatches | 11; | Indels | 2; | Gaps | 2; |
|---------|-----|--------------|----|------------|-----|--------|----|------|----|

RESULT 15
ASLJCY

R;Tristem, M.; Hill, F.; Karpas, A.
J. Gen. Virol. 72, 721-724, 1991

A;Molecule type: DNA
A;Residues: 1-104 <TRI>

C;Cross-References: UNIPROT:P24111; GB:D00835; NID:g313166; PID:g22147
C;Genetics:
A;Gene: vpr
C;Superfamily: AIDS vpr protein

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|---|--|
| DT | 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) |
| DE | Vpr protein. |
| GN | Name=vpr; |
| OS | Human immunodeficiency virus 1. |
| OC | Viruses; Retroid viruses; Retroviridae; Lentivirus. |
| OX | NCBI_TaxID=11676; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=86259728; PubMed=3014529; |
| RA | Willley R.L., Rutledge R.A., Dias S., Folke T., Theodore T., |
| RA | Buckler C.E., Martin M.A.; |
| RT | "Identification of conserved and divergent domains within the envelope |
| RT | gene of the acquired immunodeficiency syndrome retrovirus."; |
| RL | Proc. Natl. Acad. Sci. U.S.A. 83:5038-5042(1986). |
| DR | EMBL; M38431; AAB04039.1; -; |
| DR | HSSP; P12520; IDSJ. |
| DR | InterPro; IPR000012; RetroV_Vpr/X. |
| DR | Pfam; PF00522; VPR; 1. |
| DR | PRINTS; PR00444; HIVPRVPX. |
| KW | AIDS. |
| SQ | SEQUENCE 96 AA; 11377 MW; 58BC535543D87250 CRC64; |
| Query Match 100.0%; Score 262; DB 2; Length 96; | |
| Best Local Similarity 100.0%; Pred. No. 1.2e-24; | |
| Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Qy | 1 MEQAPDQGQREPYNEWTLELLBELKSEAVRHPRIWLNLGQHIY 47 |
| Db | 1 MEQAPDQGQREPYNEWTLELLBELKSEAVRHPRIWLNLGQHIY 47 |
| RESULT 3 | |
| Q99DD7 | ID |
| AC | Q99DD7; PRELIMINARY; PRT; 96 AA. |
| DT | 01-JUN-2001 (TrEMBLrel. 17, Created) |
| DT | 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) |
| DT | 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) |
| DE | Vpr protein. |
| GN | Name=vpr; |
| OS | Human immunodeficiency virus 1. |
| OC | Viruses; Retroid viruses; Retroviridae; Lentivirus. |
| OX | NCBI_TaxID=11676; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=21268767; PubMed=11375060; |
| RA | Halani N., Wang B., Ge Y.C., Gharpure H., Hira S., Saksena N.K.; |
| RT | "Changing epidemiology of HIV type 1 infections in India: evidence of |
| RT | subtype B introduction in Bombay from a common source."; |
| RL | AIDS Res. Hum. Retroviruses 17:637-642(2001). |
| DR | EMBL; AF316101; AAK11289.1; -; |
| DR | HSSP; P12520; IDSJ. |
| DR | InterPro; IPR000012; RetroV_Vpr/X. |
| DR | Pfam; PF00522; VPR; 1. |
| KW | AIDS. |
| SQ | SEQUENCE 96 AA; 11372 MW; 58BC5358EB286D4F CRC64; |
| Query Match 99.6%; Score 261; DB 2; Length 96; | |
| Best Local Similarity 97.9%; Pred. No. 1.7e-24; | |
| Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | |
| Qy | 1 MEQAPDQGQREPYNEWTLELLBELKSEAVRHPRIWLNLGQHIY 47 |
| Db | 1 MEQAPDQGQREPYNEWTLELLBELKSEAVRHPRIWLNLGQHIY 47 |
| RESULT 4 | |
| Q99DD8 | ID |
| AC | Q99DD8; PRELIMINARY; PRT; 96 AA. |
| DT | 01-JUN-2001 (TrEMBLrel. 17, Created) |
| DT | 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) |

| | |
|-----------------------|--|
| DE | Vpr protein (Fragment). |
| GN | Name=vpr; |
| OS | Human immunodeficiency virus 1. |
| OC | Viruses; Retroid viruses; Retroviridae; Lentivirus. |
| NCBI_TaxID=11676; | |
| [1] | |
| RN | SEQUENCE FROM N.A. |
| RP | MEDLINE=96325222; PubMed=9658150; |
| RX | Yedavalli V.R.; Chappay C.; Ahmad N.; |
| RT | "Maintenance of an intact human immunodeficiency virus type 1 vpr gene |
| RA | following mother-to-infant transmission."; |
| RL | J. Virol. 72:6937-6943(1998). |
| RR | EWBL; AF042912; AAC41079.1; - |
| DR | InterPro; IPR000012; Retrov_Vpr/X. |
| DR | Pfam; PF00522; VPR; 1. |
| DR | PRINTS; PR00444; HIVVPRVPX. |
| KW | AIDS. |
| FT | NON TER 96 96 |
| SQ | SEQUENCE 96 AA; 11416 MW; DB95484EC487F220 CRC64; |
| Query Match | 98.9%; Score 259; DB 2; Length 96; |
| Best Local Similarity | 97.9%; Pred. No. 2.9e-24; |
| Matches | 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0; |
| Oy | 1 MEQAPDQGQPREPYNWTLELLEELKSEAVRHPRIWLNLGHYIY 47 |
| Db | 1 MEQAPDQGQPREPYNWTLELLEELKNEAVRHPRIWLNLGHYIY 47 |
| | |
| RESULT 7 | |
| OS89603 | PRELIMINARY; PRT; 96 AA. |
| ID | OS89603 |
| AC | OS89603; |
| DT | 01-NOV-1998 (TrEMBLrel. 08, Created) |
| DT | 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) |
| DT | 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) |
| DE | Vpr protein (Fragment). |
| GN | Name=vpr; |
| OS | Human immunodeficiency virus 1. |
| OC | Viruses; Retroid viruses; Retroviridae; Lentivirus. |
| NCBI_TaxID=11676; | |
| [1] | |
| RN | SEQUENCE FROM N.A. |
| RP | MEDLINE=96325222; PubMed=9658150; |
| RX | Yedavalli V.R.; Chappay C.; Ahmad N.; |
| RT | "Maintenance of an intact human immunodeficiency virus type 1 vpr gene |
| RA | following mother-to-infant transmission."; |
| RL | J. Virol. 72:6937-6943(1998). |
| DR | EWBL; AF042913; AAC41080.1; - |
| DR | InterPro; IPR000012; Retrov_Vpr/X. |
| DR | Pfam; PF00522; VPR; 1. |
| DR | PRINTS; PR00444; HIVVPRVPX. |
| KW | AIDS. |
| FT | NON TER 96 96 |
| SQ | SEQUENCE 96 AA; 11446 MW; DB9552FECC3808241 CRC64; |
| Query Match | 98.9%; Score 259; DB 2; Length 96; |
| Best Local Similarity | 97.9%; Pred. No. 2.9e-24; |
| Matches | 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0; |
| Oy | 1 MEQAPDQGQPREPYNWTLELLEELKSEAVRHPRIWLNLGHYIY 47 |
| Db | 1 MEQAPDQGQPREPYNWTLELLEELKNEAVRHPRIWLNLGHYIY 47 |
| | |
| RESULT 8 | |
| OS89604 | PRELIMINARY; PRT; 96 AA. |
| ID | OS89604 |
| AC | OS89604; |
| DT | 01-NOV-1998 (TrEMBLrel. 08, Created) |
| DT | 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) |
| DT | 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) |
| DE | Vpr protein (Fragment). |

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R., Chappey C., Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042919; AAC41085.1; -
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGQHIY 47
|||||
Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGQHIY 47

RESULT 11

O89609
ID O89609 PRELIMINARY; PRT; 96 AA.
AC O89609;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R., Chappey C., Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042920; AAC41086.1; -
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGQHIY 47
|||||
Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGQHIY 47

RESULT 12

O89610
ID O89610 PRELIMINARY; PRT; 96 AA.
AC O89610;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R., Chappey C., Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042921; AAC41087.1; -
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGQHIY 47
|||||
Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGQHIY 47

RESULT 13

O89611
ID O89611 PRELIMINARY; PRT; 96 AA.
AC O89611;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R., Chappey C., Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042922; AAC41088.1; -
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGQHIY 47
|||||
Db 1 MEQAPEDQGPQREPYNEWTLLEELKSEAVRHPFRIWLHNLGQHIY 47

RESULT 14

O89612
ID O89612 PRELIMINARY; PRT; 96 AA.
AC O89612;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vpr protein (fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

```
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R., Chappey C., Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042923; AAC41089.1; -.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQGPQEPYNWTLLELLEKSEAVRHPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGQGPQEPYNWTLLELLEKSEAVRHPRIWLHNLGQHIY 47

RESULT 15
O89613
ID O89613 PRELIMINARY; PRT; 96 AA.
AC O89613;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein (Fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98325222; PubMed=9658150;
RA Yedavalli V.R., Chappey C., Ahmad N.;
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene
following mother-to-infant transmission.";
RL J. Virol. 72:6937-6943(1998).
DR EMBL; AF042924; AAC41090.1; -.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW AIDS.
FT NON TER 96
SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQGPQEPYNWTLLELLEKSEAVRHPRIWLHNLGQHIY 47
Db 1 MEQAPEDQGQGPQEPYNWTLLELLEKSEAVRHPRIWLHNLGQHIY 47
```

Search completed: October 18, 2004, 18:47:36
Job time : 59.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:31:42 ; Search time 64.3125 Seconds
(without alignments)
273.318 Million cell updates/sec

Title: US-09-913-927D-3

Perfect score: 254

Sequence: 1 ETYGDWAGVEAIRILQQL.....RHSRIGVTRQRRARNGASRS 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 254 | 100.0 | 49 | 3 AAB10687 | Aab10687 HIV-1 reg |
| 2 | 254 | 100.0 | 96 | 2 AAR48963 | Aar48963 HIV VPr. |
| 3 | 254 | 100.0 | 96 | 2 AAW53040 | Aaw53040 HIV-1 pol |
| 4 | 254 | 100.0 | 96 | 3 AAB10049 | Aab10049 HIV-1 vpr |
| 5 | 254 | 100.0 | 96 | 3 AAB10685 | Aab10685 HIV-1 reg |
| 6 | 254 | 100.0 | 96 | 5 AAE16129 | Aae16129 Human imm |
| 7 | 254 | 100.0 | 96 | 5 ABP56175 | Abp56175 HIV-1 vir |
| 8 | 254 | 100.0 | 96 | 5 AAU90187 | Aau90187 HIV-1 Vpr |
| 9 | 254 | 100.0 | 96 | 7 ADD01277 | Add01277 HIV-1 Vpr |
| 10 | 254 | 100.0 | 96 | 8 ADF46812 | Adf46812 HIV-1 Vpr |
| 11 | 254 | 100.0 | 96 | 8 ABM79669 | Abm79669 HIV-1 Vpr |
| 12 | 253 | 99.6 | 96 | 8 ADP20070 | Adp20070 Human imm |
| 13 | 250 | 98.4 | 95 | 8 ADP81477 | Adp81477 HIV-1 vpr |
| 14 | 250 | 98.4 | 96 | 2 AAR94544 | Aar94544 Native Vp |
| 15 | 250 | 98.4 | 96 | 3 AAY53247 | Aay53247 HIV-1 LAI |
| 16 | 249 | 98.0 | 96 | 6 ABR55491 | Abr55491 Amino aci |
| 17 | 249 | 98.0 | 96 | 8 ADP20078 | Adp20078 Human imm |
| 18 | 244 | 96.1 | 96 | 3 AAB69306 | Aab69306 HIV-1 non |
| 19 | 243 | 95.7 | 3032 | 8 ADP81468 | Adp81468 Lymphaden |
| 20 | 243 | 95.7 | 3033 | 7 ADA49379 | Ada49379 Lymphaden |
| 21 | 242 | 95.3 | 96 | 2 AAR10175 | Aar10175 Rap (R) p |
| 22 | 241 | 94.9 | 96 | 2 AAR12258 | Aar12258 HIV-1 str |
| 23 | 238 | 93.7 | 96 | 3 AAB69304 | Aab69304 HIV-1 non |
| 24 | 238 | 93.7 | 96 | 3 AAB69308 | Aab69308 HIV-1 non |
| 25 | 236 | 92.9 | 96 | 1 AAP81856 | Aap81856 Sequence |

ALIGNMENTS

RESULT 1

AAB10687

ID AAB10687 standard; peptide; 49 AA.

XX AC AAB10687;

XX XX 19-JAN-2001 (first entry)

DE HIV-1 regulatory virus protein R peptide sVpr48-96.

XX Regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity;

KW structural analysis; cell cycle arrest.

XX OS Synthetic.

OS Human immunodeficiency virus 1.

XX WO200049038-A2.

XX PD 24-AUG-2000.

XX PF 19-FEB-2000; 2000WO-DE000525.

XX PR 19-FEB-1999; 99DE-01008752.

PR 19-FEB-1999; 99DE-01008766.

XX (SCHU/) SCHUBERT U.

PA (HENK/) HENKLEIN P.

PA (WRAY/) WRAY V.

XX Schubert U, Henklein P, Wray V;

XX WPI; 2000-565367/52.

XX New synthetic peptides from the Vpr protein of human immune deficiency virus, useful e.g. for therapy and diagnosis, have good solubility in water.

XX Claim 3.3; Page 5; 35pp; German.

XX This invention describes novel synthetic peptides (I) derived from the regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-1) which have antiviral activity and can be used for gene therapy. (I) is used for therapeutic and/or diagnostic purposes, especially in biological assays, for development of serological tests or enzyme-linked immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in blood), to raise specific antibodies and antisera (especially those reactive with specific epitopes), and as antiviral agents. (I) can also be used in screening for potential Vpr antagonists (i.e. compounds that

Aab86169 HIV-1 sub
Aap81863 Sequence
Aaw72995 HIV isola
Aab69301 HIV-1 non
Aab69309 HIV-1 non
Aar10174 Rap (R) p
Adp84803 HIV-1 hyb
Abm79665 HIV Vpr52
Aau84393 HIV VPr c
Aaw99812 HIV-1 Vpr
Aaw99829 HIV Vpr p
Abb79952 Beta-lact
Aaw99817 HIV alpha
Aaw99818 HIV A308
Aaw99816 HIV E21, 2
Aaw99819 HIV A30L
Aaw99815 HIV Vpr w
Ado52527 HIV-1 rec
Ado52552 HIV-1 rec
Aab69303 HIV-1 non

CC modulate interaction of Vpr with cellular factors, transcription-
 CC activating properties of Vpr, transport of Vpr and its incorporation into
 CC viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-
 CC channel activities of Vpr. (I) is used to establish cell or animal
 CC models for studying pathogenicity of Vpr, for structural analysis of Vpr
 CC and its domains, for in vitro assembly of new vectors for gene therapy,
 CC in vitro or in vivo, for complementing the function of Vpr-defect mutants
 CC in cell cultures, and to reduce flexibility of Vpr induced by the N-
 CC terminal domain. Synthetic (II), are soluble in water and can be
 CC aggregated as highly concentrated solutions (mmolar) without protein
 CC resonance, X-ray or circular dichroism techniques. (I) adopt a folded
 CC structure, have biological activity comparable to that of viral Vpr, and
 CC can be produced, at high purity, on the milligram scale. This sequence
 CC represents the synthetic HIV-1 derived Vpr peptide svpr48-96 which is
 CC used in the method of the invention

XX Sequence 49 AA;
 SQ Query Match 100.0%; Score 254; DB 3; Length 49;
 Best Local Similarity 100.0%; Pred. No. 7e-30; Mismatches 0; Indels 0; Gaps 0;
 Matches 49; Conservative 0;
 QY 1 EYGDWTAGVEAIRILQLLFIHFRIGCRHSRIGVTRQRRNGASRS 49
 |||||
 DB 1 EYGDWTAGVEAIRILQLLFIHFRIGCRHSRIGVTRQRRNGASRS 49

RESULT 2
 AAR48963
 ID AAR48963 standard; protein; 96 AA.

XX AAR48963;
 DT 25-MAR-2003 (revised)
 DT 12-SEP-1994 (first entry)
 XX HIV VPR.
 DE HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;
 KW naturally occurring virus; NOV; translation; replication; infectivity;
 KW hepatitis B; HIV-2; HIV; flip-over PCR.
 XX Synthetic.
 XX WO9403596-A1.
 XX 17-FEB-1994.
 XX 30-JUL-1993; 93WO-US007179.
 XX 30-JUL-1992; 92US-00921104.
 XX (UYHA-) UNIV HAWAII.

XX Hu W, Wang J;
 XX WPI; 1994-065685/08.
 DR N-PSDB; AAQ48962.
 XX New antisense viruses and anti-sense-ribosome viruses - used for treating
 PT or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.
 XX Disclosure; Page 111; 167pp; English.
 CC This sequence represents the "perfect" VPR protein encoded by the PCR
 CC fragment of pX-CS which encoded the truncated gag gene and the "perfect"
 CC vpr gene. The cDNA fragment encoding this protein was used to produce the
 CC antisense virus of the invention. Antisense or truncated RNAs expressed
 CC by these viruses bind to the mRNAs expressed by the naturally occurring
 CC viruses (NOVs) and prevent the mRNAs from being translated into proteins,
 CC thereby preventing the NOV from replicating. The antisense viruses
 CC maintain the infectivity of the NOVs, allowing antisense RNAs to reach

CC the mRNAs of the natural viruses. Antisense viruses such as these may be
 CC used for treating or preventing a viral infection, particularly HIV-1,
 CC HIV-2 or SIV infection or hepatitis B infection. (Updated on 25-MAR-2003
 CC to correct PN field.)

XX Sequence 96 AA;
 SQ Query Match 100.0%; Score 254; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 1.5e-29; Mismatches 0; Indels 0; Gaps 0;
 Matches 49; Conservative 0;
 QY 1 EYGDWTAGVEAIRILQLLFIHFRIGCRHSRIGVTRQRRNGASRS 49
 |||||
 DB 48 EYGDWTAGVEAIRILQLLFIHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 3
 AAW53040
 ID AAW53040 standard; peptide; 96 AA.

XX AAW53040;
 AC AAW53040;
 DT 17-OCT-2003 (revised)
 DT 17-JUL-1998 (first entry)
 XX HIV-1 polypeptide.
 DE Recombinant plant virus; HIV-1; protein production; immunisation;
 KW fusion capsid protein; alfalfa mosaic virus; ilarvirus; pathogen;
 KW rhadovirus.
 XX Human immunodeficiency virus 1.
 OS WO9808375-A1.
 XX 05-MAR-1998.
 XX 28-AUG-1997; 97WO-US015200.
 XX 28-AUG-1996; 96US-00704856.
 XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Koprowski H, Hooper DC, Yusibov V, Modeleka A;
 XX WPI; 1998-179070/16.
 XX Production of poly:peptide(s), particularly for use in vaccines - by
 PT expression as fusion proteins with plant virus capsid protein in plant
 PT cells infected with virus.
 XX Disclosure; Page 4; 63pp; English.

XX This sequence is a HIV-1 polypeptide that can be used in a recombinant
 CC plant virus used in the process of the invention. The process is for
 CC administering a polypeptide to an animal comprising: (a) infecting a
 CC plant cell with recombinant plant virus nucleic acid that will be
 CC processed in a plant cell to produce a fusion capsid protein (FCP), the
 CC FCP comprises a plant virus capsid protein (PVCp) and a polypeptide that
 CC is not a PVCp, the PVCp being an alfalfa mosaic virus (AMV) capsid
 CC protein (CP) or ilarvirus CP thereby creating a infected cell; (b)
 CC culturing the infected cell, or a derivative cell derived from the
 CC infected cell, under conditions where the infected cell or derivative
 CC cell makes the FCP; and (c) administering the FCP or a portion to an
 CC animal. The recombinant plant virus can also be used for production of
 CC polypeptides. The method is used particularly for the production of
 CC polypeptides which can be used for immunisation against pathogens such as
 CC rhadovirus or HIV. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 96 AA;
 SQ Query Match 100.0%; Score 254; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 1.5e-29;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
 |||||
 Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 4
 AAB10049
 ID AAB10049 standard; protein; 96 AA.
 XX AAB10049;
 AC AAB10049;
 XX 12-SEP-2003 (revised)
 DT 02-NOV-2000 (first entry)
 XX HIV-1 vpr protein.
 DE HIV-1 vpr protein.
 XX Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic; gene therapy;
 KW treatment; infectious disease; HIV; AIDS; neoplasm; carcinoma; melanoma;
 KW vpr protein.
 XX Human immunodeficiency virus 1.
 OS Human immunodeficiency virus 1.
 XX EP1006196-A2.
 PN 07-JUN-2000.
 XX 25-NOV-1999; 99EP-00250415.
 PF 26-NOV-1998; 98DE-01056463.
 XX (PETT-) PETTE INST HEINRICH.
 PA Von Laer MD;
 PI WPI; 2000-378268/33.
 DR N-PSDB; AAA40298, AAB10053, AAB10054.
 XX New retroviral packing cell useful as pharmaceutical carrier in gene
 PT therapy for treatment of HIV and neoplasms, comprises retroviral genes
 PT and glycoproteins.
 PS Disclosure; Page 44; 69pp; German.
 XX This invention describes a novel retroviral packing cell (I), comprising
 CC the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV
 CC coding gene gp, or a part of these. The products of the invention have
 CC anti-HIV and cytostatic activity and can be used for gene therapy. (I) is
 CC useful for in vitro infection of cells, especially hematopoietic stem
 CC cells, for expression of transgenes in cells and as a pharmaceutical
 CC carrier for gene therapy. (I) is therefore useful in the treatment of
 CC infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and
 CC other diseases. This sequence represents the Human Immunodeficiency virus
 CC (HIV-1) vpr protein described in the method of the invention. (Updated on
 CC 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 96 AA;

Query Match 100.0%; Score 254; DB 3; Length 96;
 Best Local Similarity 100.0%; Pred. No. 1.5e-29;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
 |||||
 Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 5
 AAB10685
 ID AAB10685 standard; peptide; 96 AA.
 XX AAB10685;
 AC AAB10685;

XX 19-JAN-2001 (first entry)
 DT HIV-1 regulatory virus protein R peptide svpr1-96.
 DE HIV-1 regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity;
 XX structural analysis; cell cycle arrest.
 KW Synthetic.
 KW Human immunodeficiency virus 1.
 OS WO200049038-A2.
 XX 24-AUG-2000.
 XX 19-FEB-2000; 2000WO-DE5000525.
 PF 19-FEB-1999; 99DE-01008752.
 PR 19-FEB-1999; 99DE-01008766.
 XX (SCHU/) SCHUBERT U.
 PA (HENK/) HENKLEIN P.
 PA (WRAY/) WRAY V.
 XX Schubert U, Henklein P, Wray V;
 PI WPI; 2000-565367/52.
 DR New synthetic peptides from the Vpr protein of human immune deficiency
 PT virus, useful e.g. for therapy and diagnosis, have good solubility in
 PT water.
 XX Claim 3.1; Page 5; 35pp; German.

XX This invention describes novel synthetic peptides (I) derived from the
 CC regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-
 CC 1) which have antiviral activity and can be used for gene therapy. (I) is
 CC used for therapeutic and/or diagnostic purposes, especially in biological
 CC assays, for development of serological tests or enzyme-linked
 CC immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in
 CC blood), to raise specific antibodies and antisera (especially those
 CC reactive with specific epitopes), and as antiviral agents. (I) can also
 CC be used in screening for potential Vpr antagonists (i.e. compounds that
 CC modulate interaction of Vpr with cellular factors, transcription-
 CC activating properties of Vpr, transport of Vpr and its incorporation into
 CC viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-
 CC channel activities of Vpr). (I) is used to establish cell or animal
 CC models for studying pathogenicity of Vpr, for structural analysis of Vpr
 CC and its domains, for in vitro assembly of new vectors for gene therapy,
 CC in vitro or in vivo, for complementing the function of Vpr-defect mutants
 CC in cell cultures, and to reduce flexibility of Vpr induced by the N-
 CC terminal domain. Synthetic (I), are soluble in water and can be
 CC formulated as highly concentrated solutions (mmolar) without protein
 CC aggregation, so are well suited to analysis by nuclear magnetic
 CC resonance, x-ray or circular dichroism techniques. (I) adopt a folded
 CC structure, have biological activity comparable to that of viral Vpr, and
 CC can be produced, at high purity, on the milligram scale. This sequence
 CC represents the synthetic HIV-1 derived Vpr peptide svpr1-96 which is used
 CC in the method of the invention

XX Sequence 96 AA;
 SQ Query Match 100.0%; Score 254; DB 3; Length 96;
 Best Local Similarity 100.0%; Pred. No. 1.5e-29;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
 |||||
 Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 6
 AAB16129

AAE16129 standard; protein; 96 AA.
AAE16129;
29-AUG-2003 (revised)
26-MAR-2002 (first entry)
Human immunodeficiency virus type 1 (HIV-1) sVpr protein.
Human immunodeficiency virus type 1; HIV-1; auxiliary protein; cancer;
Vpr protein; regulatory protein; pathogen; cell proliferation; therapy;
dysregulated cell growth; hyperproliferative cell disorder; malignancy;
radiation therapy; psoriasis; transgene expression; immune response;
cytostatic; apoptotic.
Human immunodeficiency virus 1.
Key Location/Qualifiers
Region 17..29
/label= Alpha_1_helix
Region 36..47
/label= Alpha_2_helix
Region 53..78
/label= Alpha_3_helix
WO200190159-A2.
29-NOV-2001.
23-MAY-2001; 2001WO-US016943.
23-MAY-2000; 2000US-0206610P.
09-FEB-2001; 2001US-0267827P.
20-APR-2001; 2001US-00839329.
(GLAD-) GLADSTONE INST J DAVID.
(SCHU/) SCHUBERT U.
(HENK/) HENKLEIN P.
Schubert U, Henklein P, Sherman MP, Greene WC, De Noronha CMC;
WPI; 2002-083087/11.
Delivering molecule into cell for inhibiting cell proliferation and
killing target cell, comprises contacting cell with Vpr polypeptide,
regulatory protein encoded by HIV type 1, alone or conjugated to
molecule.
Example 1; Fig 1A; 72pp; English.
The present invention relates to compositions comprising Vpr polypeptides
conjugated to a therapeutic molecule. Vpr polypeptides are regulatory or
auxiliary proteins encoded by a lentivirus, human immunodeficiency virus
type 1 (HIV-1). The invention also relates to a method for delivering a
molecule into a cell which comprises contacting the cell with a conjugate
comprising a Vpr polypeptide conjugated to the molecule. The method is
useful for delivering a polypeptide, polynucleotide (DNA or RNA) or a
toxin into a cell, preferably a cancer cell, or a cell infected with a
pathogen such as lentivirus, HIV or retrovirus, bacterium or a parasite.
Compositions comprising Vpr polypeptide conjugated to a toxin is useful
for killing a cancer cell or a cell infected with a pathogen where the
toxin is further conjugated to a regulatory molecule and the contact with
the target cell exerts an effect on the regulatory molecule that results
in activation of the toxin. The method is useful for inhibiting cell
proliferation and treating a disorder associated with dysregulated cell
growth in a subject. Vpr polypeptides when administered alone are useful
for increasing sensitivity to radiation therapy in a subject undergoing
radiation therapy. They can also be used to treat hyperproliferative cell
disorders such as malignancies, psoriasis and other disorders associated
with dysregulated cell growth. Vpr polypeptides conjugated to a
regulatory moiety is useful for modulating the expression of a transgene
in a cell. Vpr polypeptides alone or conjugated to an antigen is useful
for increasing an immune response. The present sequence is synthetic Vpr

(sVpr) protein from HIV-1. (Updated on 29-AUG-2003 to standardise OS
field)
XX Sequence 96 AA;
Query Match 100.0%; Score 254; DB 5; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 49
|||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 96
|||||
RESULT 7
ABP56175
ID ABP56175 standard; peptide; 96 AA.
XX
AC ABP56175;
XX
DT 29-AUG-2003 (revised)
DT 28-MAR-2003 (first entry)
XX
DE HIV-1 viral protein R (Vpr) amino acid sequence.
XX
KW Mitochondrial membrane permeabilisation; mitochondrion; PTPC;
KW permeability transition pore complex; virucide; neuroprotective;
KW vasotrophic; cytostatic; infection; cell death regulation; apoptosis;
KW mitochondrial permeability transition pore complex modulator; cancer;
KW apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200261105-A2.
XX
PD 08-AUG-2002.
XX
PF 01-FEB-2002; 2002WO-EP001633.
XX
PR 02-FEB-2001; 2001US-0265594P.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Edelman L, Jacotot E, Briand J;
XX
XX
DR WPI; 2002-619260/66.
XX
PT New chimeric bifunctional molecules that target specific cells and
PT regulate the apoptosis function of the permeability transition pore
PT complex of the mitochondria, useful for treating or preventing e.g.
PT cancer or ischemia.
PS Disclosure; Page 13; 76pp; English.
XX
CC The present invention describes a chimeric bifunctional molecule (I)
CC comprising at least a first functional molecule covalently linked to a
CC second functional molecule, which is able to modulate the activity of the
CC permeability transition pore complex (PTPC) of the mitochondria. (I) has
CC the function of specifically targeting and entering a tissue cell
CC population. The second functional molecule has the function of
CC specifically targeting, and inducing or preventing the death of the cells
CC by apoptosis by regulating the opening or the closing of the PTPC of the
CC mitochondria or its fragment. (I) has virucide, neuroprotective,
CC vasotropic and cytostatic activities, and can be used as a mitochondrial
CC permeability transition pore complex (PTPC) modulator. (I) is useful for
CC treating or preventing a pathological infection or disease. (I) is also
CC useful for regulating cell death regulatory molecules, specifically the
CC apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia,
CC neurodegenerative diseases, fulminant hepatitis or viral infections. The
CC present sequence represents the HIV-1 viral protein R (Vpr) amino acid
CC sequence, which is given in the exemplification of the present invention.
CC (Updated on 29-AUG-2003 to standardise OS field)

```

XX SQ Sequence 96 AA;
Query Match 100.0%; Score 254; DB 5; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRNGASRS 49
Dy 48 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 8
ID AAU80187 standard; protein; 96 AA.
AC AAU80187;
XX 29-AUG-2003 (revised)
DT 15-JUL-2002 (first entry)
XX HIV-1 Vpr protein.
XX HIV-1; acquired immunodeficiency syndrome; AIDS; Vpr.
XX Human immunodeficiency virus 1.
XX Key Location/Qualifiers
FT Misc-difference 45 /note= "Encoded by CAT"
XX JP2002085099-A.
XX 26-MAR-2002.
XX 14-SEP-2000; 2000JP-00280851.
XX 14-SEP-2000; 2000JP-00280851.
XX (KOKU-) KOKURITSU YOB0 EISEI KENKYUSHO.
PA (ORIY) ORIENTAL YEAST CO LTD.
XX WPI; 2002-378279/41.
DR N-PSDB; ABK50386.
XX Detection of immunodeficiency virus by detecting the presence of Vpr protein.
XX Disclosure; Page 8; 17pp; Japanese.
XX The invention relates to a method for detecting immunodeficiency virus in a sample in which the presence of Vpr (not defined) protein in the sample is detected. Also included are a kit for use in the above detecting a method containing a cell and a pigment, and a method for screening a compound promoting or inhibiting the intake of a substance having a molecular weight (M.W.) of 300 to 3000 in which the promotion or the inhibition of intake of the substance by the presence of a test compound is used as the index in the intake of the substance to the cell by a treatment using a sample containing Vpr protein. The method is used for detecting immunodeficiency virus (e.g. Human immunodeficiency virus-1, the causative agent of acquired immunodeficiency virus syndrome, AIDS) in a sample. The present sequence represents HIV-1 Vpr. (Updated on 29-AUG-2003 to standardise OS field)
XX Sequence 96 AA;
Query Match 100.0%; Score 254; DB 5; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRNGASRS 49
Dy 48 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRNGASRS 96

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RESULT 9
ADD01277
ID ADD01277 standard; protein; 96 AA.
XX ADD01277;
XX 01-JAN-2004 (first entry)
XX HIV-1 Vpr CyPA protein binding motif.
XX lentivirus protein R; Vpr; inhibitor; cellular chaperone; folding; stability; cyclophilin A; CyPA; cell-cycle arrest; apoptosis; glucocorticoid receptor coactivation; anti-HIV; neurotropic; nephrotropic; antileptic; antiretroviral; AIDS; infection; HIV-induced dementia; lipodystrophy syndrome; lipid metabolism; HIV-associated nephropathy.
XX Human immunodeficiency virus 1.
OS WO2003038032-A2.
XX 08-MAY-2003.
XX 25-OCT-2002; 2002WO-DE004052.
XX 25-OCT-2001; 2001DE-01053902.
XX (MEDI-) MEDICIS VENTURES MANAGEMENT GMBH.
XX Will H, Tessmer U, Bruns K;
XX WPI; 2003-430506/40.
XX Agent for inhibiting lentivirus Vpr protein, useful for treatment and prevention of infection by human immune deficiency virus, is inhibitor of chaperone enzyme.
XX Disclosure; Fig 4; 41pp; German.
XX This invention describes a novel agent (A), for inhibiting the primate lentivirus protein R (Vpr) of HIV-1 or -2, or simian immune deficiency virus, comprising an inhibitor (I) of cellular chaperones (II) that are essential for proper folding, stability and, thus, biological function of Vpr. The inhibitor is useful for inhibiting interaction of Vpr with cyclophilins include cyclosporin A, FK506, rapamycin and the non-immunosuppressive compounds SDZ NIM811 and/or sangliferin A. Vpr first binds to cyclophilin A (CyPA) to regulate the trans conformation of proline peptidyl bonds in the N-terminus of Vpr. The inhibitor prevents cis-trans rearrangement, specifically of pro residues at positions 5, 10, 14 and 35 of Vpr. The inhibitor may also act by a process in which CyPA co-translationally regulates expression, folding and stability of Vpr and this stabilizing process is active in cells transfected with the specified viruses, with DNA that encodes Vpr, or with recombinant Vpr-encoding retro, adeno, vaccinia or baculo viruses. All essential functions of Vpr (induction of cell-cycle arrest, apoptosis, increased viral production and co-activation of glucocorticoid receptors) are inhibited. The products of the invention have anti-HIV, neurotropic, nephrotropic and antileptic activity. The inhibitor may be used in combination with other antiretroviral agents; blockers of reverse transcription and/or protease; genetically based antiretroviral therapies, intracellular immunization and administration of anti-HIV gene in stem cells and/or peripheral CD4+ lymphocytes, especially in advanced stages of disease. The agent of the invention is used to prevent and treat lentiviral infections, specifically AIDS or HIV infections (including where asymptomatic), also HIV-induced dementia (by inhibiting infection of neurons, glial cells and endothelial cells in cerebral capillaries), HIV-associated lipodystrophy syndrome or other disorders of lipid metabolism and HIV-associated nephropathy, also to prevent systemic infection immediately after exposure to HIV, e.g. needle pricks with HIV-contaminated blood. This sequence represents the CyPA binding fragment at the N-terminal of the HIV-1(NL4-3) Vpr protein.
XX

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SQ Sequence 96 AA;
Query Match      100.0%; Score 254; DB 7; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
    |||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 10
ADF46812
ID ADF46812 standard; protein; 96 AA.
XX
AC ADF46812;
XX
DT 12-FEB-2004 (first entry)
XX
DE HIV-1 Vpr protein.
XX
KW virus protein R; Vpr; functional analysis.
XX
OS Human immunodeficiency virus 1.
XX
PN JP2003259881-A.
XX
PD 16-SEP-2003.
XX
PF 12-MAR-2002; 2002JP-00066938.
XX
PR 12-MAR-2002; 2002JP-00066938.
XX
PA (ORIY ) ORIENTAL YEAST CO LTD.
PA (NAKA/) NAKAMURA T.
XX
DR WPI; 2004-026590/03.
DR N-PSDB; ADF46813.
XX
PT Producing recombinant virus protein R (Vpr), useful in promoting
PT immunodeficiency virus reproduction, involves transforming a host cell
PT with an expression vector for the protein.
XX
PS Claim 1; SEQ ID NO 1; 14pp; Japanese.
XX
CC The invention relates to a method of producing a recombinant HIV-1 virus
CC protein R (Vpr) protein or a protein having one or more substitutions,
CC additions or alterations and having biological activity, by transforming
CC a host Escherichia coli cell with an expression vector containing the
CC gene encoding Vpr, and culturing the transformed cell. The method is
CC useful for producing recombinant Vpr protein. The protein is useful for
CC promoting the reproduction of immunodeficiency virus in cell, tissue or
CC organ derived from an organism. The protein is useful for functional
CC analysis of the Vpr protein. This sequence represents the HIV-1 Vpr
CC protein.
XX
SQ Sequence 96 AA;

Query Match      100.0%; Score 254; DB 8; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
    |||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 11
ABM79669
ID ABM79669 standard; protein; 96 AA.
XX
AC ABM79669;
XX

22-APR-2004 (first entry)
HIV-1 Vpr protein.
HIV; Vpr; modulator; anti-HIV; virucide.
Human immunodeficiency virus type 1.
WO2003076621-A2.
18-SEP-2003.
07-MAR-2003; 2003WO-CA000325.
08-MAR-2002; 2002US-0362384P.
(UYMO-) UNIV MONTREAL.
Cohen EA, Yao X, Belhumeur P, Lemay J;
WPI; 2004-042337/04.
New polypeptides that bind to viral Vpr protein, useful for treatment,
prevention, diagnosis and prognosis of immune deficiency virus infection.
Example 20; Page 33-34; 143pp; English.
The present invention relates to peptide which are capable of binding to
the HIV protein Vpr and/or modulates Vpr-related activity. Such peptides
are used for prevention, treatment, diagnosis and prognosis of Vpr-
related diseases, particularly lentiviral infection (specifically HIV-1
or -2, or simian immune deficiency virus), for modulating, particularly
inhibiting, Vpr-related activities and for detecting Vpr in a sample.
Nucleic acids encoding such peptides and cells that contain this nucleic
acid can also be used therapeutically. The present sequence is a protein
of relevance to the invention
SQ Sequence 96 AA;

Query Match      100.0%; Score 254; DB 8; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
    |||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 12
ADP20070
ID ADP20070 standard; protein; 96 AA.
XX
AC ADP20070;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human immunodeficiency virus 1 isolate JRCSEF vpr protein.
XX
KW immunogenic mutant HIV gp120; human immunodeficiency virus; HIV; gp120;
KW immunogenic; vaccine; HIV neutralising antibody; anti-HIV;
KW HIV binding agent; immunisation; HIV-1; infection; HIV-1 isolate JRCSEF;
KW VPR.
XX
OS Human immunodeficiency virus 1.
XX
PN WO2004053100-A2.
XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-US039534.
XX
PR 11-DEC-2002; 2002US-0432869P.
PR 24-APR-2003; 2003US-0465350P.

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XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Wilson I, Pantophlet R;
 PI
 XX WPI; 2004-480933/45.
 DR N-PSDB; ADP20074.
 DR GENBANK; M38429.
 XX
 XX Immunogenic mutant HIV-1 gp120 polypeptide, and antibodies raised against
 PT the polypeptide, useful preventing or treating human immunodeficiency
 PT virus (HIV) infection, especially HIV-1 infection.
 XX
 XX Disclosure; Page 138; 149pp; English.
 PS
 XX The present invention describes an immunogenic mutant HIV gp120
 CC polypeptide that can stimulate a neutralising antibody response against a
 CC human immunodeficiency virus (HIV). Also described: (1) an immunogenic
 CC mutant HIV-1 gp120 polypeptide (Ia) that can stimulate a neutralising
 CC antibody response against a panel of HIV-1 comprising HIV-1 primary
 CC isolates of at least two different clades, where the mutant gp120 has at
 CC least one amino acid mutation in at least one epitope of the HIV-1 gp120
 CC polypeptide specifically bound by a neutralising antibody, which reduces
 CC binding affinity of the non-neutralising antibody; (2) an immunogenic
 CC mutant HIV-1 gp120 polypeptide (Ib) having at least one amino acid
 CC mutation in at least one epitope of the gp120 polypeptide specifically
 CC bound by a non-neutralising antibody; (3) a vaccine (II) comprising one
 CC or more (Ia); (4) an antiserum (III) obtained by using (Ib) or (II); (5)
 CC an isolated HIV neutralising antibody (IV) fraction obtained by using
 CC (Ib) or (II); (6) a substantially purified HIV neutralising antibody (V)
 CC obtained by using (Ib) or (II); (7) ameliorating (M1) HIV-1 infection in
 CC a subject, by administering an HIV neutralising antibody produced in
 CC response to (Ib); (8) preventing (M2) HIV-1 infection or ameliorating HIV
 CC -1 infection in a human subject, involves administering HIV-1
 CC neutralising antibodies to the subject, where the HIV-1 neutralising
 CC antibodies comprise antibodies stimulated in response to (II); (9) HIV
 CC neutralising antibodies (VI) produced by using (Ib); (10) isolated HIV
 CC neutralising antibodies (VII) obtained by using (Ib); and (11) isolated
 CC HIV-1 neutralising antibodies obtained by harvesting spleen and lymph
 CC nodes from the mouse immunised by (II). (Ia) and (Ib) have anti-HIV
 CC activities, and can be used in vaccines and in HIV binding agents. (Ia)
 CC and (Ib) are useful for inducing antibodies that can neutralise HIV-1
 CC which involves immunising a subject with a (Ia) or (Ib). The antibodies
 CC are useful for preventing or ameliorating HIV, especially HIV-1,
 CC infection in a subject. The present sequence represents an HIV-1 isolate
 CC JRCSEF vpr protein sequence, which is given in the exemplification of the
 CC present invention.
 XX
 XX Sequence 96 AA;
 SQ

Query Match 99.6%; Score 253; DB 8; Length 96;
 Best Local Similarity 98.0%; Pred. No. 2.1e-29;
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49
 |||||
 Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 96
 |||||

RESULT 13
 ADP81477
 ID ADP81477 standard; protein; 95 AA.
 XX
 AC ADP81477;
 XX
 DT 12-AUG-2004 (first entry)
 DE HIV-1 vpr protein.
 XX
 XX vaccine; vpr; HIV-1; HIV infection; ds; gene.
 XX
 OS Human immunodeficiency virus 1.
 XX

PN US6706268-B1.
 XX
 PD 16-MAR-2004.
 XX
 PF 13-NOV-2000; 2000US-00709316.
 XX
 PR 18-OCT-1984; 84PR-00016013.
 PR 16-NOV-1984; 84GB-00029099.
 PR 30-AUG-1985; 85US-00771248.
 PR 22-FEB-1988; 88US-00158652.
 PR 05-NOV-1992; 92US-00953060.
 PR 14-FEB-1994; 94US-00195024.
 PR 31-DEC-1997; 97US-00344449.
 XX
 XX (INSP) INST PASTEUR.
 PA (CNRS) CENT NAT RECH SCI.
 XX
 PI Alison M, Sonigo P, Stewart C, Danos O, Main-Hobson S;
 DR WPI; 2004-236717/22.
 XX N-PSDB; ADP81478.
 DR
 XX New purified peptide encoded by the vpr gene of HIV-1, useful for
 PT preparing a composition for diagnosing or treating HIV infection.
 PT
 XX Claim 1; Col 10; 37pp; English.
 PS
 XX The invention relates to a new purified peptide encoded by the vpr gene
 CC of HIV-1 is free of particles of the virus. The peptide is useful for
 CC preparing a composition for diagnosing or treating HIV infection. The
 CC present sequence represents the HIV-1 vpr protein.
 XX
 XX Sequence 95 AA;
 SQ

Query Match 98.4%; Score 250; DB 8; Length 95;
 Best Local Similarity 98.0%; Pred. No. 5.7e-29;
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49
 |||||
 Db 47 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 95
 |||||

RESULT 14
 AAR94544
 ID AAR94544 standard; protein; 96 AA.
 XX
 AC AAR94544;
 XX
 DT 16-OCT-2003 (revised)
 DT 17-OCT-1996 (first entry)
 XX
 XX Native Vpr protein from HIV-1 LAI strain isolate.
 DE
 XX Native; Vpr protein; HIV-1 LAI strain isolate; chimeric molecule;
 KW chimeric; infection; replication; reduction; RNase; protease;
 KW virion assembly; morphogenesis; steric hindrance inducer; targeted;
 KW mature virion; structural organisation; gene therapy;
 KW functional integrity.
 XX
 OS Human immunodeficiency virus 1.
 OS
 XX WO9607741-A1.
 XX
 PD 14-MAR-1996.
 XX
 PF 07-SEP-1995; 95WO-CA000510.
 XX
 PR 07-SEP-1994; 94US-00301915.
 XX
 XX (UYMO-) UNIV MONTREAL.
 PA
 XX Cohen EA, Bergeron D, Checroune F, Yao X, Pignac-Kobinger G;
 PI

XX WPI; 1996-171615/17.
 XX Targeting mature HIV virion(s) using HIV Vpr, Vpx or p6 proteins - for
 PT affecting structural organisation or function or for inhibiting
 PT replication.
 XX
 XX Claim 8; Page 43; 68pp; English.
 XX
 CC The present sequence is the native Vpr protein from the HIV-1 LAI strain
 CC isolate, which can be used in the development of a chimaeric mol.
 CC comprising the present sequence and another mol., pref. a HIV infectivity
 CC or replication reducing protein fragment, i.e. a RNase and/or protease, a
 CC virion assembly and/or morphogenesis steric hindrance inducer and/or an
 CC affector of a viral protein interaction responsible for viral infectivity
 CC and/or replication. The chimaeric mol. can be specifically targeted into
 CC the mature HIV-1 virion, to affect its structural organisation and/or
 CC functional integrity, i.e. gene therapy of HIV-1 infection. Vpr protein
 CC fragments can also be used to prevent viral replication by interfering
 CC with the protein interactions responsible for Vpr incorporation into the
 CC mature HIV-1 genome. (Updated on 16-Oct-2003 to standardise OS field)
 XX
 XX Sequence 96 AA;
 SQ

Query Match 98.4%; Score 250; DB 2; Length 96;
 Best Local Similarity 98.0%; Pred. No. 5.8e-29;
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIIIRILQQLFIHFRIGCRHSRIGVTRQRRNAGSRS 49
 Db 48 ETYGDWAGVEAIIIRILQQLFIHFRIGCRHSRIGVTRQRRNAGSRS 96

RESULT 15
 AAY53247
 ID AAY53247 standard; protein; 96 AA.
 AC AAY53247;
 XX
 XX 12-SEP-2003 (revised)
 DT 17-JUL-2000 (first entry)
 DE HIV-1 LAI strain Vpr protein SEQ ID NO:1.
 KW HIV-1; HIV-2; virion; Vpr; Vpx; p6; chimeric; infection; anti-HIV;
 KW gene therapy.
 XX Human immunodeficiency virus 1.
 OS
 XX US6043081-A.
 PN
 XX 28-MAR-2000.
 PD
 XX 07-SEP-1995; 95US-00524694.
 XX
 XX 07-SEP-1994; 94US-00301915.
 XX
 XX (UYMO-) UNIV MONTREAL.
 PA
 XX Yao X, Pignac-Kobinger G, Checroune F, Cohen EA, Bergeron D;
 FI WPI; 2000-270343/23.
 XX
 XX Expression vector useful for reducing infectivity of HIV or for targeting
 PT into HIV virions, comprises nucleic acid segment encoding recombinant or
 PT chimeric protein comprising a Vpr/Vpx virion incorporation domain.
 XX
 XX Claim 1; Col 7-8; 32pp; English.
 PS
 XX The present invention describes an expression vector (1) comprising a
 CC nucleic acid segment encoding a recombinant protein for interfering with
 CC the incorporation of native Vpr/Vpx into HIV-1 or HIV-2 virion or a
 CC chimeric protein that is incorporated into an HIV-1 or HIV-2 virion,

CC operably linked to a promoter. Also described are: (1) an isolated
 CC eukaryotic or prokaryotic cell transformed with (1); (2) a composition
 CC for reducing infectivity of HIV-1 or HIV-2 in vitro comprising an
 CC effective amount of (1) in association with a pharmaceutically acceptable
 CC carrier; and (3) a composition for targeting into an HIV-1 or HIV-2
 CC virion comprising an effective amount of (1) in association with a
 CC pharmaceutically acceptable carrier. (1) has anti-HIV activity and can be
 CC used in gene therapy. (1) is useful for reducing infectivity of HIV in
 CC vitro and for targeting into an HIV-1 or HIV-2 virion. The present
 CC sequence represents the Vpr protein from an HIV-1 strain, which is used
 CC in the exemplification of the present invention. (Updated on 12-SEP-2003
 CC to standardise OS field)
 XX
 XX Sequence 96 AA;
 SQ

Query Match 98.4%; Score 250; DB 3; Length 96;
 Best Local Similarity 98.0%; Pred. No. 5.8e-29;
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIIIRILQQLFIHFRIGCRHSRIGVTRQRRNAGSRS 49
 Db 48 ETYGDWAGVEAIIIRILQQLFIHFRIGCRHSRIGVTRQRRNAGSRS 96

Search completed: October 18, 2004, 18:45:33
 Job time : 65.3125 secs

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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:42:45 ; Search time 28.5833 Seconds
(without alignments)
113.688 Million cell updates/sec

Title: US-09-913-927D-3

Perfect score: 254

Sequence: 1 ETYGDWAGVEAIRILQQL.....RHSRIGVTRRRNGASRS 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 254 | 100.0 | 96 | 4 | US-09-309-572-19 |
| 2 | 254 | 100.0 | 96 | 4 | US-09-718-096-19 |
| 3 | 254 | 100.0 | 96 | 4 | US-09-839-329-1 |
| 4 | 250 | 98.4 | 96 | 2 | US-08-301-915-1 |
| 5 | 250 | 98.4 | 96 | 3 | US-08-524-694A-1 |
| 6 | 250 | 98.4 | 96 | 4 | US-09-454-156A-1 |
| 7 | 249 | 98.0 | 96 | 3 | US-08-704-856C-15 |
| 8 | 249 | 98.0 | 96 | 4 | US-09-242-881-15 |
| 9 | 210.5 | 82.9 | 95 | 4 | US-09-319-588C-10 |
| 10 | 197 | 77.6 | 100 | 4 | US-09-462-917A-118 |
| 11 | 192 | 75.6 | 100 | 4 | US-09-462-917A-115 |
| 12 | 179 | 70.5 | 100 | 4 | US-09-462-917A-115 |
| 13 | 172 | 67.7 | 93 | 4 | US-09-462-917A-117 |
| 14 | 132 | 52.0 | 78 | 3 | US-09-124-900-5 |
| 15 | 131 | 51.6 | 72 | 2 | US-08-301-915-4 |
| 16 | 131 | 51.6 | 72 | 3 | US-08-524-694A-4 |
| 17 | 131 | 51.6 | 72 | 4 | US-09-454-156A-4 |
| 18 | 123 | 48.4 | 24 | 4 | US-09-839-329-2 |
| 19 | 119.5 | 47.0 | 3077 | 6 | 5223423-2 |
| 20 | 117 | 46.1 | 100 | 4 | US-09-206-551-49 |
| 21 | 116 | 45.7 | 105 | 2 | US-08-301-915-2 |
| 22 | 116 | 45.7 | 105 | 3 | US-08-524-694A-2 |
| 23 | 116 | 45.7 | 105 | 4 | US-09-454-156A-2 |
| 24 | 105 | 41.3 | 105 | 2 | US-08-659-251-9 |
| 25 | 105 | 41.3 | 105 | 3 | US-09-256-490-9 |
| 26 | 105 | 41.3 | 105 | 5 | PCT-US96-11445-9 |
| 27 | 94 | 37.0 | 18 | 4 | US-09-839-329-3 |

Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 38, Appl
Sequence 10, Appl
Sequence 106, App
Sequence 128, App
Sequence 7, Appl
Sequence 37, Appl
Sequence 5911, Ap
Sequence 24912, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 29104, A
Sequence 29150, A
Sequence 25736, A
Sequence 30, Appl
Sequence 30, Appl

28 74 29.1 13 2 US-08-484-905-58
29 74 29.1 13 3 US-08-481-985B-58
30 74 29.1 13 3 US-08-370-476-58
31 74 29.1 13 3 US-08-992-877-38
32 73 28.7 16 5 PCT-US94-02191-10
33 72 28.3 15 4 US-09-009-953-106
34 70 27.6 15 4 US-09-009-953-128
35 63 24.8 16 5 PCT-US94-02191-7
36 62 24.4 14 3 US-08-992-877-37
37 62 24.4 112 4 US-09-621-976-5911
38 57 22.4 218 4 US-09-252-991A-24912
39 54.5 21.5 723 4 US-09-849-334-2
40 54.5 21.5 723 4 US-10-274-878-2
41 53 20.9 245 4 US-09-252-991A-29404
42 52.5 20.7 265 4 US-09-252-991A-29150
43 52.5 20.7 651 4 US-09-252-991A-25736
44 52 20.5 9 1 US-07-841-662-30
45 52 20.5 9 1 US-08-209-797-30

ALIGNMENTS

RESULT 1

US-09-309-572-19

; Sequence 19, Application US/09309572

; Patent No. 6440730

; GENERAL INFORMATION:

; APPLICANT: Heinrich-Pette-Institut

; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV

; FILE REFERENCE: P50489

; CURRENT APPLICATION NUMBER: US/09/309,572

; CURRENT FILING DATE: 1999-05-11

; EARLIER APPLICATION NUMBER: DE 198 56 463

; EARLIER FILING DATE: 1998-11-26

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

; FEATURE:

; OTHER INFORMATION: vpr protein

; US-09-309-572-19

Query Match 100.0%; Score 254; DB 4; Length 96;

Best Local Similarity 100.0%; Pred. No. 76-31; Indels 0; Gaps 0;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLFIHFRIGCRHSRIGVTRRRNGASRS 49

Db 48 ETYGDWAGVEAIRILQQLFIHFRIGCRHSRIGVTRRRNGASRS 96

RESULT 2

US-09-718-096-19

; Sequence 19, Application US/09718096

; Patent No. 6585763

; GENERAL INFORMATION:

; APPLICANT: Von Laer, Meike-Dorothee

; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV

; FILE REFERENCE: 35-195

; CURRENT APPLICATION NUMBER: US/09/718,096

; CURRENT FILING DATE: 2000-11-22

; PRIOR APPLICATION NUMBER: DE 19856463.5

; PRIOR FILING DATE: 1998-11-26

; PRIOR APPLICATION NUMBER: EP 99250415.9

; PRIOR FILING DATE: 1999-11-25

; PRIOR APPLICATION NUMBER: US 09/309,572

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

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;
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: vpr protein
US-09-718-096-19

Query Match      100.0%; Score 254; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 7e-31;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 3
US-09-839-329-1
; Sequence 1, Application US/09839329
; Patent No. 6664040
; GENERAL INFORMATION:
; APPLICANT: Michael P. Sherman
; APPLICANT: Warner C. Greene
; APPLICANT: Carlos M.C. de No. 6664040ohna
; APPLICANT: Ulrich Schubert
; APPLICANT: Peter Henklein
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
; FILE REFERENCE: GSC 30448.91-US-U2
; CURRENT APPLICATION NUMBER: US/09/839,329
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/206,610
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/267,827
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide of regulatory virus proteins R
; OTHER INFORMATION: (vpr) of human immunodeficiency virus type 1
; OTHER INFORMATION: (HIV-1)
US-09-839-329-1

Query Match      100.0%; Score 254; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 7e-31;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 4
US-08-301-915-1
; Sequence 1, Application US/08301915
; Patent No. 5861161
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
```

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;
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,915
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
US-08-301-915-1

Query Match      98.4%; Score 250; DB 2; Length 96;
Best Local Similarity 98.0%; Pred. No. 2.8e-30;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 5
US-08-524-694A-1
; Sequence 1, Application US/08524694A
; Patent No. 6043081
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED
; TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,694A
; FILING DATE: September 7, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
```



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; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-524-694A-1

Query Match          98.4%; Score 250; DB 3; Length 96;
Best Local Similarity 98.0%; Pred. No. 2.8e-30;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 96

RESULT 6
US-09-454-156A-1
; Sequence 1, Application US/09454156A
; Patent No. 6468539
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECKROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454,156A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/301,915
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-454-156A-1

Query Match          98.4%; Score 250; DB 4; Length 96;
Best Local Similarity 98.0%; Pred. No. 2.8e-30;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 96

US-09-454-156A-1
; Sequence 1, Application US/09454156A
; Patent No. 6468539
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECKROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454,156A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/301,915
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-454-156A-1

Query Match          98.4%; Score 250; DB 3; Length 96;
Best Local Similarity 98.0%; Pred. No. 2.8e-30;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 96

RESULT 7
US-08-704-856C-15
; Sequence 15, Application US/08704856C
; Patent No. 6042832
; GENERAL INFORMATION:
; APPLICANT: KOPROWSKI, Hilary
; APPLICANT: YUSIBOV, Vidadi
; APPLICANT: HOOPER, Douglas, C.
; APPLICANT: MODELSKA, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
; TITLE OF INVENTION: Coat Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,856C
; FILING DATE: 28-Aug-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; HYPOTHETICAL: N
; US-08-704-856C-15

Query Match          98.0%; Score 249; DB 3; Length 96;
Best Local Similarity 98.0%; Pred. No. 4e-30;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRARGASRS 96

RESULT 8
US-09-242-881-15
; Sequence 15, Application US/09242881
; Patent No. 6448070
; GENERAL INFORMATION:
; APPLICANT: KOPROWSKI, Hilary
; APPLICANT: YUSIBOV, Vidadi
; APPLICANT: HOOPER, Douglas, C.
; APPLICANT: MODELSKA, Anna
; TITLE OF INVENTION: Polypeptides Fused with Plant Virus
; TITLE OF INVENTION: Coat Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allan H. Fried & Associates
; STREET: 1525 Locust Street, 15th Floor
; CITY: Philadelphia
; US-09-242-881-15
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; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19102
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Corel WordPerfect
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/242,881
; FILING DATE: 25-Feb-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,856
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fried, Allan H.
; REGISTRATION NUMBER: 31,253
; REFERENCE/DOCKET NUMBER: T19-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 732-7090
; TELEFAX: (215) 732-7090
;
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; HYPOTHETICAL: N
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-242-881-15

Query Match 98.0%; Score 249; DB 4; Length 96;
Best Local Similarity 98.0%; Pred. No. 4e-30;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRARNGASRS 96

RESULT 9
US-09-319-588C-10
; Sequence 10, Application US/09319588C
; Patent No. 6509018
; GENERAL INFORMATION:
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INSERM
; APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS
; APPLICANT: INSTITUT PASTEUR
; APPLICANT: MAUCLEIRE, Philippe
; APPLICANT: LOUSSERT-AJAKA, Ibtissam
; APPLICANT: SIMON, Francois
; APPLICANT: SARAGOSTI, Sentob
; APPLICANT: BARRE-SINOUSSE, Françoise
; TITLE OF INVENTION: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATIONS.
; FILE REFERENCE: 598US12
; CURRENT APPLICATION NUMBER: US/09/319,588C
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: FR96/15087
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-319-588C-10

Query Match 82.9%; Score 210.5; DB 4; Length 95;
Best Local Similarity 85.4%; Pred. No. 2.7e-24;
Matches 41; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 2 TYGDTWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRARNGASRS 96
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Db 49 TYGDTWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRARNGTSRS 95

RESULT 10
US-09-462-917A-118
; Sequence 118, Application US/09462917A
; Patent No. 6511801
; GENERAL INFORMATION:
; APPLICANT: Delaporte, Eric
; APPLICANT: Peeters, Martine
; APPLICANT: Saman, Eric
; APPLICANT: Vanden Haesevelde, Marlen
; TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof
; FILE REFERENCE: INNS:014 11362.0014.NPUS00
; CURRENT APPLICATION NUMBER: US/09/462,917A
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: PCT/EP98/04522
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 118
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Human
US-09-462-917A-118

Query Match 77.6%; Score 197; DB 4; Length 100;
Best Local Similarity 73.6%; Pred. No. 3.2e-22;
Matches 39; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

QY 1 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRARNGSRS 100

RESULT 11
US-09-462-917A-115
; Sequence 115, Application US/09462917A
; Patent No. 6511801
; GENERAL INFORMATION:
; APPLICANT: Delaporte, Eric
; APPLICANT: Peeters, Martine
; APPLICANT: Saman, Eric
; APPLICANT: Vanden Haesevelde, Marlen
; TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof
; FILE REFERENCE: INNS:014 11362.0014.NPUS00
; CURRENT APPLICATION NUMBER: US/09/462,917A
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: PCT/EP98/04522
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Human
US-09-462-917A-115

Query Match 75.6%; Score 192; DB 4; Length 100;
Best Local Similarity 71.7%; Pred. No. 1.8e-21;
Matches 38; Conservative 4; Mismatches 7; Indels 4; Gaps 1;

QY 1 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRARNGSRS 100

RESULT 12
US-09-462-917A-116
; Sequence 116, Application US/09462917A
; Patent No. 6511801
; GENERAL INFORMATION:
; APPLICANT: Delaporte, Eric
```

```
; APPLICANT: Peeters, Martine
; APPLICANT: Saman, Eric
; TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof
; FILE REFERENCE: INNS:014 11362.0014.NPUS00
; CURRENT APPLICATION NUMBER: US/09/462.917A
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: PCT/EP98/04522
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Human
US-09-462-917A-116

Query Match 70.5%; Score 179; DB 4; Length 100;
Best Local Similarity 65.4%; Pred. No. 1.7e-19;
Matches 34; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY 1 ETYGDWTWAGVEAIRILQQLLFHFRIGCRHSRIGV---TRQRRARNGASR 48
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 48 DTYGDTWGWMAIRILQQLMFAHFRIGCRHSRIGVPSNTRGRNGSSR 99

RESULT 13
US-09-462-917A-117
; Sequence 117, Application US/09462917A
; Patent No. 6511801
; GENERAL INFORMATION:
; APPLICANT: Delaporte, Eric
; APPLICANT: Peeters, Martine
; APPLICANT: Saman, Eric
; APPLICANT: Vanden Haesevelde, Marlen
; TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof
; FILE REFERENCE: INNS:014 11362.0014.NPUS00
; CURRENT APPLICATION NUMBER: US/09/462.917A
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: PCT/EP98/04522
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Human
US-09-462-917A-117

Query Match 67.7%; Score 172; DB 4; Length 93;
Best Local Similarity 83.8%; Pred. No. 1.8e-18;
Matches 31; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ETYGDWTWAGVEAIRILQQLLFHFRIGCRHSRIGVT 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 48 ETYGDWTWGWMAIRILQQLMFAHFRIGCRHSRIGIT 84

RESULT 14
US-09-124-900-5
; Sequence 5, Application US/09124900
; Patent No. 6268484
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; APPLICANT: BUCHACHER, Andrea
; APPLICANT: ERNST, Wolfgang
; APPLICANT: BALLAUN, Claudia
; APPLICANT: PURTSCHER, Martin
; APPLICANT: TRKOLA, Alexandra
; APPLICANT: PREDL, Renate
; APPLICANT: SCHMATZ, Christine
; APPLICANT: KLIMA, Annelies
; APPLICANT: STEINDL, Franz
```

```
; APPLICANT: MUSTER, Thomas
; TITLE OF INVENTION: HIV-Vaccines
; FILE REFERENCE: 1939-112P
; CURRENT APPLICATION NUMBER: US/09/124,900
; CURRENT FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/EP95/01481
; PRIOR FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-124-900-5

Query Match 52.0%; Score 132; DB 3; Length 78;
Best Local Similarity 96.2%; Pred. No. 1.7e-12;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTWAGVEAIRILQQLLFHFR 26
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 48 ETYGDWTWAGVEAIRILQQLLFHFRQ 73

RESULT 15
US-08-301-915-4
; Sequence 4, Application US/08301915
; Patent No. 5861161
; GENERAL INFORMATION:
; APPLICANT: COHEN, Eric A.
; APPLICANT: BERGERON, Dominique
; APPLICANT: CHECROUNE, Florent
; APPLICANT: YAO, Xiao-Jian
; APPLICANT: PIGNAC-KOBINGER, Gary
; TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS
; TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,915
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-301-915-4

Query Match 51.6%; Score 131; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ETYGDWAGVEAIRILOQLLFHF 25
Db 48 ETYGDWAGVEAIRILOQLLFHF 72

Search completed: October 18, 2004, 18:49:23
Job time : 29.5833 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:43:30 ; Search time 88.8125 Seconds
(without alignments)
178.383 Million cell updates/sec

Title: US-09-913-927D-3
Perfect score: 254
Sequence: 1 ETYGDWTWAGVEAIRILQQL.....RHSRIGVTRQRRANGASRS 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 254 | 100.0 | 96 | 9 | US-09-839-329-1 |
| 2 | 254 | 100.0 | 96 | 14 | Sequence 1, Appl1 |
| 3 | 254 | 100.0 | 96 | 14 | Sequence 272, App |
| 4 | 240 | 94.5 | 96 | 14 | Sequence 284, App |
| 5 | 239 | 94.1 | 96 | 14 | Sequence 272, App |
| 6 | 238 | 93.7 | 96 | 14 | Sequence 285, App |
| 7 | 235 | 92.5 | 96 | 14 | Sequence 284, App |
| 8 | 235 | 92.5 | 96 | 14 | Sequence 272, App |
| 9 | 234 | 92.1 | 96 | 14 | Sequence 278, App |
| 10 | 234 | 92.1 | 96 | 14 | Sequence 263, App |
| 11 | 234 | 92.1 | 96 | 14 | Sequence 273, App |
| 12 | 233 | 91.7 | 96 | 14 | Sequence 276, App |
| 13 | 233 | 91.7 | 96 | 14 | Sequence 264, App |
| 14 | 233 | 91.7 | 96 | 14 | Sequence 265, App |
| | | | | | Sequence 266, App |

| | | | | | | |
|----|-------|------|-----|----|--------------------|-------------------|
| 15 | 233 | 91.7 | 96 | 14 | US-10-190-435-270 | Sequence 270, App |
| 16 | 233 | 91.7 | 96 | 14 | US-10-190-435-271 | Sequence 271, App |
| 17 | 232 | 91.3 | 96 | 14 | US-10-190-435-256 | Sequence 256, App |
| 18 | 232 | 91.3 | 96 | 14 | US-10-190-435-257 | Sequence 257, App |
| 19 | 231 | 90.9 | 96 | 14 | US-10-190-435-283 | Sequence 283, App |
| 20 | 231 | 90.9 | 96 | 15 | US-10-296-734-4 | Sequence 4, Appl1 |
| 21 | 231 | 90.9 | 96 | 15 | US-10-296-734-1475 | Sequence 1475, Ap |
| 22 | 229 | 90.2 | 96 | 14 | US-10-190-435-258 | Sequence 258, App |
| 23 | 229 | 90.2 | 96 | 14 | US-10-190-435-259 | Sequence 259, App |
| 24 | 229 | 90.2 | 96 | 14 | US-10-190-435-260 | Sequence 260, App |
| 25 | 229 | 90.2 | 96 | 14 | US-10-190-435-267 | Sequence 267, App |
| | 228.5 | 90.0 | 362 | 15 | US-10-469-199-2 | Sequence 2, Appl1 |
| 26 | 227 | 89.4 | 96 | 14 | US-10-190-435-268 | Sequence 268, App |
| 27 | 227 | 89.4 | 96 | 14 | US-10-190-435-269 | Sequence 269, App |
| 28 | 227 | 89.4 | 96 | 16 | US-10-325-468-11 | Sequence 11, Appl |
| 29 | 225 | 88.6 | 96 | 16 | US-10-325-468-36 | Sequence 36, Appl |
| 30 | 225 | 88.6 | 96 | 14 | US-10-190-435-275 | Sequence 275, App |
| 31 | 224 | 88.2 | 96 | 14 | US-10-190-435-282 | Sequence 282, App |
| 32 | 224 | 88.2 | 96 | 14 | US-10-190-435-277 | Sequence 277, App |
| 33 | 222 | 87.4 | 96 | 14 | US-10-190-435-261 | Sequence 261, App |
| 34 | 218 | 85.8 | 96 | 14 | US-10-190-435-280 | Sequence 280, App |
| 35 | 216 | 85.0 | 96 | 14 | US-10-190-435-254 | Sequence 254, App |
| 36 | 215 | 84.6 | 96 | 14 | US-10-190-435-255 | Sequence 255, App |
| 37 | 215 | 84.6 | 96 | 14 | US-10-190-435-279 | Sequence 279, App |
| 38 | 213 | 83.9 | 96 | 14 | US-10-301-661A-10 | Sequence 10, Appl |
| 39 | 210.5 | 82.9 | 95 | 14 | US-10-190-435-281 | Sequence 281, App |
| 40 | 210 | 82.7 | 96 | 14 | US-10-059-261-229 | Sequence 229, App |
| 41 | 207 | 81.5 | 45 | 14 | US-10-059-261-293 | Sequence 293, App |
| 42 | 207 | 81.5 | 44 | 14 | US-09-971-980-51 | Sequence 51, Appl |
| 43 | 201 | 79.1 | 44 | 9 | US-10-296-734-1476 | Sequence 1476, Ap |
| 44 | 201 | 79.1 | 45 | 14 | US-10-059-261-231 | Sequence 231, App |
| 45 | 199 | 78.3 | 45 | 14 | | |

ALIGNMENTS

RESULT 1

US-09-839-329-1
; Sequence 1, Application US/09839329
; Publication No. US20020022027A1
; GENERAL INFORMATION:
; APPLICANT: Michael P. Sherman
; APPLICANT: Warner C. Greene
; APPLICANT: Carlos M.C. de No. 6664040ohna
; APPLICANT: Ulrich Schubert
; APPLICANT: Peter Henklein
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
; FILE REFERENCE: A MOLECULE INTO A CELL
; FILE REFERENCE: G&C 30448.91-US-U2
; CURRENT FILING DATE: 2001-04-20
; CURRENT FILING DATE: 2001-04-20
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/267,827
; PRIOR APPLICATION NUMBER: 60/267,827
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide of regulatory virus proteins R
; OTHER INFORMATION: (vpr) of human immunodeficiency virus type 1
; OTHER INFORMATION: (HIV-1)
US-09-839-329-1

Query Match 100.0%; Score 254; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETYGDWTWAGVEAIRILQQLFIHFHFRIGCRHSRIGVTRQRRANGASRS 49
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Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

RESULT 2

; Sequence 272, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 272
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-059-261-272

Query Match 100.0%; Score 254; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 49
|||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

RESULT 3

US-10-190-435-284
; Sequence 284, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr HXB2
US-10-190-435-284

Query Match 100.0%; Score 254; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 49
|||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

RESULT 4

US-10-190-435-272

; Sequence 272, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 272
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV005-81
US-10-190-435-272

Query Match 94.5%; Score 240; DB 14; Length 96;
Best Local Similarity 89.8%; Pred. No. 1.6e-26;
Matches 44; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 49
|||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

RESULT 5

US-10-190-435-285
; Sequence 285, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 285
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus
US-10-190-435-285

Query Match 94.1%; Score 239; DB 14; Length 96;
Best Local Similarity 91.8%; Pred. No. 2.2e-26;
Matches 45; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 49
|||||
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRNGASRS 96

RESULT 6

US-10-190-435-262
; Sequence 262, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.

; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 319
; SEQ ID NO 262
; TYPE: PRT
; LENGTH: 96
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV004-45
US-10-190-435-262

Query Match 93.7%; Score 238; DB 14; Length 96;
Best Local Similarity 89.8%; Pred. No. 3e-26;
Matches 44; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTGWGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWTGWGVEAIRVLQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 7

US-10-190-435-274
; Sequence 274, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 319
; SEQ ID NO 274
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV006-9
US-10-190-435-274

Query Match 92.5%; Score 235; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 8.2e-26;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTGWGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWTGWGVEAIRVLQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 8

US-10-190-435-278
; Sequence 278, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; TYPE: PRT
; LENGTH: 96
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr 301905-Ind
US-10-190-435-278

Query Match 92.5%; Score 235; DB 14; Length 96;
Best Local Similarity 89.8%; Pred. No. 8.2e-26;
Matches 44; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ETYGDWTGWGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWTGWGVEAIRVLQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 9

US-10-190-435-263
; Sequence 263, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 263
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV001-2
US-10-190-435-263

Query Match 92.1%; Score 234; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 1.1e-25;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTGWGVEAIRILQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 49
Db 48 ETYGDWTGWGVEAIRVLQQLLFTHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 10

US-10-190-435-273
; Sequence 273, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 273
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV012-4
US-10-190-435-273

Query Match          92.1%; Score 234; DB 14; Length 96;
Best Local Similarity 91.7%; Pred. No. 1.1e-25;
Matches 44; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYGDTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRARNGASRS 49
Db 49 TYGDTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRARNGASRS 96

RESULT 11
US-10-190-435-276
; Sequence 276, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 276
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr 92BR025
US-10-190-435-276

Query Match          92.1%; Score 234; DB 14; Length 96;
Best Local Similarity 91.7%; Pred. No. 1.1e-25;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRARNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRARNGASRS 96

RESULT 12
US-10-190-435-264
; Sequence 264, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 264
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV018-7
US-10-190-435-264

Query Match          91.7%; Score 233; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 1.6e-25;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRARNGASRS 49
Db 48 DTYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRARNGASRS 96

RESULT 13
US-10-190-435-265
; Sequence 265, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 265
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV018-8
US-10-190-435-265

Query Match          91.7%; Score 233; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 1.6e-25;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRARNGASRS 49
Db 48 DTYGDWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRRRARNGASRS 96

RESULT 14
US-10-190-435-266
; Sequence 266, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV002-84
US-10-190-435-266

Query Match          91.7%; Score 233; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 1.6e-25;
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Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 48 DTYGDTWGWGVEAIRILQQLLFHFRIGCQHSRIGIIRRRNGASRS 96

RESULT 15
US-10-190-435-270
; Sequence 270, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 270
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr TV003-12
US-10-190-435-270

Query Match 91.7%; Score 233; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 1.6e-25;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 48 DTYGDTWGWGVEAIRILQQLLFHFRIGCQHSRIGIIRRRNGASRS 96

Search completed: October 18, 2004, 18:52:23
Job time : 89.8125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2004, 18:38:31 ; Search time 17.3542 Seconds
(without alignments)
271.671 Million cell updates/sec

Title: US-09-913-927D-3
Perfect score: 254
Sequence: 1 ETYGDWTWAGVEAIRILQQL.....RHSRIGVTRQRRRNGASRS 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 249 | 98.0 | 96 | 2 T09444 | vpr protein - huma |
| 2 | 244 | 96.1 | 96 | 2 S54380 | vpr protein - huma |
| 3 | 235 | 92.5 | 96 | 2 T01670 | vpr protein - huma |
| 4 | 233.5 | 91.9 | 95 | 2 T09383 | vpr protein - huma |
| 5 | 228.5 | 90.0 | 97 | 1 D44001 | vpr protein - huma |
| 6 | 205 | 80.7 | 96 | 1 ASLJSC | vpr protein - simi |
| 7 | 120 | 47.2 | 89 | 2 S07991 | vpr protein - simi |
| 8 | 120 | 47.2 | 101 | 2 T11563 | vpr protein - simi |
| 9 | 120 | 47.2 | 105 | 2 S53095 | vpr protein - huma |
| 10 | 118 | 46.5 | 101 | 2 S08439 | vpr protein - huma |
| 11 | 117 | 46.1 | 122 | 1 ASLJRS | vpr protein - simi |
| 12 | 116 | 45.7 | 105 | 1 ASLJRS | vpr protein - huma |
| 13 | 115 | 45.3 | 101 | 1 ASLJRS | vpr protein - simi |
| 14 | 113 | 44.5 | 104 | 1 ASLJCY | vpr protein - huma |
| 15 | 111 | 43.7 | 97 | 2 S03087 | gene R protein - h |
| 16 | 110.5 | 43.5 | 104 | 1 ASLJSY | vpr protein - huma |
| 17 | 110 | 43.3 | 105 | 1 ASLJGR | vpr protein - huma |
| 18 | 108 | 42.5 | 105 | 2 S12156 | vpr protein - huma |
| 19 | 67.5 | 26.6 | 119 | 1 ASLJXA | vpu protein - simi |
| 20 | 56.5 | 22.2 | 314 | 2 C97332 | ABC-type transport |
| 21 | 55.5 | 21.9 | 178 | 2 T42536 | hypothetical prote |
| 22 | 54.5 | 21.5 | 328 | 2 H81996 | probable integral |
| 23 | 54.5 | 21.5 | 328 | 2 H81225 | hypothetical prote |
| 24 | 54.5 | 21.5 | 454 | 2 A13467 | glycine betaine/1- |
| 25 | 53.5 | 21.1 | 275 | 2 B55224 | hypothetical prote |
| 26 | 53.5 | 21.1 | 311 | 2 H95877 | hypothetical prote |
| 27 | 53 | 20.9 | 532 | 2 G84427 | hypothetical prote |
| 28 | 52.5 | 20.7 | 341 | 2 F69171 | conserved hypothe |
| 29 | 51.5 | 20.3 | 282 | 2 C69553 | conserved hypothe |

ALIGNMENTS

RESULT 1

T09444

vpr protein - human immunodeficiency virus type 1 (strain JRPL)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T09444

R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A;Reference number: Z16673

A;Accession: T09444

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-96 <PAN>

A;Cross-references: UNIPROT:Q75757; EMBL:U63632; NID:g1465777; PID:g1465784

C;Genetics:

A;Gene: vpr

C;Superfamily: AIDS vpr protein

Query Match 98.0%; Score 249; DB 2; Length 96;

Best Local Similarity 95.9%; Pred. No. 7.6e-28;

Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRRNGASRS 49

|||||

Db 48 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 2

S54380

vpr protein - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S54380

R;Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A;Reference number: S54377

A;Accession: S54380

A;Status: preliminary

A;Molecule type: genomic RNA

A;Residues: 1-96 <THE>

A;Cross-references: UNIPROT:P12519; EMBL:M22639; NID:g329377; PID:AAA45368.1; PID:g329377

C;Superfamily: AIDS vpr protein

Query Match 96.1%; Score 244; DB 2; Length 96;

Best Local Similarity 91.8%; Pred. No. 3.8e-27;

Matches 45; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRRNGASRS 49

|||||

Db 48 ETYGDWTWAGVEAIRILQQLLFHFHFRIGCRHSRIGVTRQRRRNGASRS 96

RESULT 3

T01670
vpr protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01670
R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates
A:Reference number: Z14389; MUID:86245056; PMID:2424612
A:Accession: T01670
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-96 <ALI>
A:Cross-references: UNIPROT:P05955; EMBL:K03456; NID:G60228; PIDN:CAA28014.1; PID:G60232
C:Superfamily: AIDS vpr protein

Query Match 92.5%; Score 235; DB 2; Length 96;
Best Local Similarity 89.8%; Pred. No. 7.2e-26;
Matches 44; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49
|||||
DB 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 96
|||||

RESULT 4

T09383
vpr protein - human immunodeficiency virus type 1 (isolate cntrl 1)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate cntrl 1
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09383
R:Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir
J. Virol. 69, 4228-4236, 1995
A:Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lon
A:Reference number: Z16654; MUID:95287475; PMID:7769682
A:Accession: T09383
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-95 <MTC>
A:Cross-references: UNIPROT:Q71925; EMBL:U24451; NID:G829440; PIDN:AAA79575.1; PID:G8294
C:Genetics:
A:Gene: vpr
C:Superfamily: AIDS vpr protein
C:Keywords: AIDS; immunodeficiency

Query Match 91.9%; Score 233.5; DB 2; Length 95;
Best Local Similarity 93.9%; Pred. No. 1.2e-25;
Matches 46; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49
|||||
DB 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 95
|||||

RESULT 5

D44001
vpr protein - human immunodeficiency virus type 1 (strain YU-2)
N:Alternate names: orf-R protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: D44001
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A:Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387; PMID:1404605
A:Accession: D44001
A:Molecule type: DNA
A:Residues: 1-97 <LIY>
A:Cross-references: UNIPROT:P35967; GB:M93258
C:Genetics:

A:Gene: vpr
C:Superfamily: AIDS vpr protein
C:Keywords: AIDS; immunodeficiency

Query Match 90.0%; Score 228.5; DB 1; Length 97;
Best Local Similarity 90.0%; Pred. No. 6e-25;
Matches 45; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49
|||||
DB 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 97
|||||

RESULT 6

ASLJSC
vpr protein - simian immunodeficiency virus SIVcpz
N:Alternate names: orf-R protein
C:Species: simian immunodeficiency virus SIVcpz
A:Note: host Pan troglodytes (chimpanzee)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S09986
R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Reference number: S09983; MUID:90259077; PMID:2188136
A:Accession: S09986
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-96 <HUE>
A:Cross-references: UNIPROT:P17287; EMBL:X52154; NID:G58866; PIDN:CAA36403.1; PID:G58870
C:Genetics:
A:Gene: vpr
C:Superfamily: AIDS vpr protein
C:Keywords: AIDS; immunodeficiency

Query Match 80.7%; Score 205; DB 1; Length 96;
Best Local Similarity 75.5%; Pred. No. 1.3e-21;
Matches 37; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 49
:|||||
DB 48 DTYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRRRRNGASRS 96
:|||||

RESULT 7

S07991
vpr protein - simian immunodeficiency virus SIVsm (isolate F236)
C:Species: simian immunodeficiency virus SIVsm
A:Note: host Cercopithecus torquatus atys (sooty mangabey)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S07991
R:Hirsch, V.M.; Olmsted, R.A.; Murphy-Corb, M.; Purcell, R.H.; Johnson, P.R.
Nature 339, 389-392, 1989
A:Title: An African primate lentivirus (SIV(sm)) closely related to HIV-2.
A:Reference number: S04237; MUID:89262053; PMID:2786147
A:Accession: S07991
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: genomic RNA
A:Residues: 1-89 <HIR>
A:Cross-references: UNIPROT:P12521; EMBL:X14307; NID:G61741; PIDN:CAA32486.1; PID:G61745
A:Note: this sequence was submitted to the EMBL Data Library, February 1989
C:Genetics:
A:Gene: vpr
C:Superfamily: AIDS vpr protein

Query Match 47.2%; Score 120; DB 2; Length 89;
Best Local Similarity 60.5%; Pred. No. 1.2e-09;
Matches 23; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTR 38
:|||||
DB 49 DRHGTLEAGELIRILQRLFIHFRSCAHSRIGQSR 86
:|||||

vpr protein - simian immunodeficiency virus (macaque isolate)
N:Alternate names: ori-R protein
C:Species: simian immunodeficiency virus, SIV
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C:Accession: E28887
R:Chakrabarti, L.; Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P.
Nature 328, 543-547, 1987
A:Title: Sequence of simian immunodeficiency virus from macaque and its relationship to
A:Reference number: A28887; MUID:87287230; PMID:3649576
A:Accession: E28887
A:Molecule type: DNA
A:Residues: 1-101 <CHA>
A:Cross-references: GB:Y00277; GB:M16403; NID:G61730; PIDN:CAA6383.1; PID:G61735
C:Genetics:
A:Gene: vpr
C:Superfamily: AIDS vpr protein
C:Keywords: AIDS; immunodeficiency

Query Match 45.3%; Score 115; DB 1; Length 101;
Best Local Similarity 66.7%; Pred. No. 7e-09;
Matches 22; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 3 YGDTWAGVEAIRILQQLFIHFRIGCRHSRIG 35
:||| | :|||: ||||| | |||||
Db 51 HGDTLEAGELIRILQALFIHFRSGCHSRIG 83

RESULT 14

ASLUCY
 vpr protein - human immunodeficiency virus type 2 (isolate CAM2/Guinea-Bissau)
 N;Alternate names: orf-R protein
 C:Species: human immunodeficiency virus type 2, HIV-2
 A:Note: host Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C:Accession: E38475; JQ0977
 R:Tristem, M.; Hill, F.; Karpas, A.
 J. Gen. Virol. 72, 721-724, 1991
 A:Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type 2
 A:Reference number: A38475; MUID:91170959; PMID:2005437
 A:Accession: E38475
 A:Molecule type: DNA
 A:Residues: 1-104 <TRI>
 A:Cross-references: UNIPROT:P24111; GB:D00835; NID:G3153166; PIDN:BAA00713.1; PID:G22147
 C:Genetics:
 A:Gene: vpr
 C:Superfamily: AIDS vpr protein
 C:Keywords: AIDS; immunodeficiency

```
Query Match      44.5%; Score 113; DB 1; Length 104;
Best Local Similarity 58.3%; Pred. No. 1.4e-08;
Matches 21; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
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QY 3 YGDTWAGVEAIRILQQLFIHFIRIGCRHSRIGVTR 38
 : ::::: | | | | |
Dd 55 HGDTLERARELINVLRALFTFRAGCNHSRIGTR 90

RESULT 15

Gene R protein - human T-cell lymphotropic virus type 4
C-Species: human T-cell lymphotropic virus type 4, HTLV-4
Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
Accession: S03067
L.I.: Lee, S.W.; Kumar, P.; Taylor, M.E.; Arya, S.K.; Shaw, G.M.
Title: Relation of HTLV-4 to simian and human immunodeficiency-associated viruses.
Reference number: S03065
A: Accession: S03067
Status: preliminary; nucleic acid sequence not shown; translation not shown
Molecule type: DNA
Residues: 1-97 <HA>
Cross-references: UNIPROT:Q85605; EMBL:X06391; NID:G61580; PIDN:CAA29689.1; PID:G61582
Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1987

C;Superfamily: AIDS vpr protein

| | | | | |
|-----------------------|------------------|--------------------|-----------|------------|
| Query Match | 43.7%; | Score 111; | DB 2; | Length 97; |
| Best Local Similarity | 63.6%; | Pred. No. 2.5e-08; | | |
| Matches | 21; Conservative | 4; Mismatches | 8; Indels | |

Qy 3 YGDTWAGVEAIRILQLQLFIHFIRIGCRHSRIG 35
 :|::|::|::|::|::|::|::|::|::|::|::|::|
Db 51 HGDLTLEGAGELIIRLQALFHFIRGCNCHSRIG 83
 :|::|::|::|::|::|::|::|::|::|::|::|

Search completed: October 18, 2004, 18:48:21
Job time : 18.3542 secs

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|-----------|--------------------|
| | Score | Match | Length | | | |
| 1 | 254 | 100.0 | 96 | 1 | VPR_HV1N5 | P12520 human immun |
| 2 | 253 | 99.6 | 96 | 1 | VPR_HV1JR | P20883 human immun |
| 3 | 253 | 99.6 | 96 | 2 | Q6SZU3 | Q6szu3 human immun |
| 4 | 253 | 99.6 | 96 | 2 | Q51BN7 | Q51bn7 human immun |
| 5 | 253 | 99.6 | 96 | 2 | AAR24628 | Aar24628 human imm |
| 6 | 252 | 99.2 | 96 | 2 | Q71267 | Q71267 human immun |
| 7 | 252 | 99.2 | 96 | 2 | Q903U7 | Q903u7 human immun |
| 8 | 251 | 98.8 | 96 | 2 | Q60440 | Q6q440 human immun |
| 9 | 251 | 98.8 | 96 | 2 | AAS86190 | Aas86190 human imm |
| 10 | 250 | 98.4 | 96 | 1 | VPR_HV1BR | P05928 human immun |
| 11 | 250 | 98.4 | 96 | 2 | Q91Q8B | Q91qb8 human immun |
| 12 | 249 | 98.0 | 96 | 1 | VPR_HV1RH | P05954 human immun |
| 13 | 249 | 98.0 | 96 | 2 | Q36203 | Q36203 human immun |
| 14 | 249 | 98.0 | 96 | 2 | Q6JN73 | Q6jn73 human immun |
| 15 | 249 | 98.0 | 96 | 2 | Q6SZU2 | Q6szu2 human immun |
| 16 | 249 | 98.0 | 96 | 2 | Q6SZU5 | Q6szu5 human immun |
| 17 | 249 | 98.0 | 96 | 2 | Q71999 | Q71999 human immun |
| 18 | 249 | 98.0 | 96 | 2 | Q72014 | Q72014 human immun |
| 19 | 249 | 98.0 | 96 | 2 | Q75757 | Q75757 human immun |
| 20 | 249 | 98.0 | 96 | 2 | Q79234 | Q79234 human immun |
| 21 | 249 | 98.0 | 96 | 2 | Q73245 | Q73245 human immun |
| 22 | 249 | 98.0 | 96 | 2 | Q7S029 | Q7seu9 human immun |
| 23 | 249 | 98.0 | 96 | 2 | Q7SV42 | Q7sv42 human immun |
| 24 | 249 | 98.0 | 96 | 2 | Q6H1N6 | Q6h1n6 human immun |
| 25 | 249 | 98.0 | 96 | 2 | Q7ZJ96 | Q7zj96 human immun |
| 26 | 249 | 98.0 | 96 | 2 | Q89636 | Q89636 human immun |
| 27 | 249 | 98.0 | 96 | 2 | Q91QA5 | Q91qa5 human immun |
| 28 | 249 | 98.0 | 96 | 2 | Q91QA6 | Q91qa6 human immun |
| 29 | 249 | 98.0 | 96 | 2 | Q91QA8 | Q91qa8 human immun |
| 30 | 249 | 98.0 | 96 | 2 | Q91QA9 | Q91qa9 human immun |
| 31 | 249 | 98.0 | 96 | 2 | Q91QAO | Q91qbo human immun |

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DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE VPR protein (R ORF protein).
GN Name=VPR;
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; M38429; AAB03747.1; -
CC DR HSP; P12520; 1BDE.
CC DR HIV; M38429; VPRJRCSF.
CC DR InterPro; IPR000012; Retrov_Vpr/X.
CC DR Pfam; PF00522; VPR; 1.
CC DR PRINTS; PR00444; HIVVPRPX.
CC KW AIDS.
SQ SEQUENCE 96 AA; 11419 MW; 06954E578BED2925 CRC64;
Query Match 99.6%; Score 253; DB 1; Length 96;
Best Local Similarity 98.0%; Pred. No. 1e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETYGDWTAGVGAIRIILQQLFIHFHRCGRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWTAGVGAIRIILQQLFIHFHRCGRHSRIGVTRQRRARNGASRS 96
RESULT 3
Q6SZU3 PRELIMINARY; PRT; 96 AA.
AC Q6SZU3;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Vpr protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Rodas B., Toro C., Paxinos E., Poveda E., Martinez-Padial M.,
RA Benito J.M., Jimenez V., Wrin T., Basani S., Soriano V.;
RT "Differences in disease progression in a cohort of long-term non-
RT progressors after more than 16 years of HIV-1 infection."
RL AIDS 18:1109-1116(2004).
DR EMBL; AY444321; AAR24628.1; -
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRPX.
DR KW AIDS.
SQ SEQUENCE 96 AA; 11353 MW; 9576F43AFEDB1244 CRC64;
Query Match 99.6%; Score 253; DB 2; Length 96;
Best Local Similarity 98.0%; Pred. No. 1e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETYGDWTAGVGAIRIILQQLFIHFHRCGRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWTAGVGAIRIILQQLFIHFHRCGRHSRIGVTRQRRARNGASRS 96
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RESULT 4
Q9IBN7 PRELIMINARY; PRT; 96 AA.
ID Q9IBN7;
AC Q9IBN7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE VPR protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Vella C., Smith M.H., Farrar G.H., Jones D.H., Daniels R.S.;
RT "A molecular and serologic study of the envelope gene of the British
RT isolate: HIV-1 GB8."
RL Vaccine 13:735-741(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=subtype B;
RX MEDLINE=91366314; PubMed=1890410;
RA Farrar G.H., Roff M.A., Amin T., Ball J., Parrett A.M.,
RA Battacharya U., Booth J., Wansbrough-Jones M.H., Greenaway P.J.;
RT "Characterisation of a series of human immunodeficiency virus isolates
RT derived sequentially from a single patient."
RL J. Med. Virol. 34:104-113(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=subtype B;
RX MEDLINE=204118939; PubMed=10954893;
RA Novelli P., Vella C., Oxford J.S., Daniels R.S.;
RT "Biological characterization of an infectious molecular clone of HIV
RT Type 1GB8."
RL AIDS Res. Hum. Retroviruses 16:1175-1178(2000).
DR EMBL; AJ271445; CAB92789.1; -
DR HSP; P12520; 1BDE.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
KW AIDS.
FT CHAIN 1 20 vif.
FT CHAIN 1 96 vpr.
FT CHAIN 91 96 tat.
SQ SEQUENCE 96 AA; 11293 MW; C00C5A439E0DD92E CRC64;
Query Match 99.6%; Score 253; DB 2; Length 96;
Best Local Similarity 98.0%; Pred. No. 1e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETYGDWTAGVGAIRIILQQLFIHFHRCGRHSRIGVTRQRRARNGASRS 49
Db 48 ETYGDWTAGVGAIRIILQQLFIHFHRCGRHSRIGVTRQRRARNGASRS 96
RESULT 5
AAR24628 PRELIMINARY; PRT; 96 AA.
ID AAR24628;
AC AAR24628;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE Vpr protein.
GN VPR.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9;
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RA Rodas B., Toro C., Paxinos E., Poveda E., Martinez-Padial M.,
RT Jimenez V., Wrin T., Bassani S., Soriano V.;
RA "Differences in disease progression in a cohort of long-term non-
RT progressors after more than 15 years of HIV-1 infection.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY44321; AAR24628.1; -.
SQ SEQUENCE 96 AA; 11353 MW; 9576F43AFEDB1244 CRC64;

Query Match 99.6%; Score 253; DB 2; Length 96;
Best Local Similarity 98.0%; Pred. No. 1e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 6
ID O71267 PRELIMINARY; PRT; 96 AA.
AC O71267
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Oelrichs R.B., McPhee D.A., Deacon N.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042103; AAD03219.1; -.
DR HSP; P12520; IDSJ.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
SQ SEQUENCE 96 AA; 11349 MW; AE455A5E25808256 CRC64;

Query Match 99.2%; Score 252; DB 2; Length 96;
Best Local Similarity 95.9%; Pred. No. 1.4e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 7
ID Q903U7 PRELIMINARY; PRT; 96 AA.
AC Q903U7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes D.I., Ashton L., Solomon A., Carr A., Cooper D., Kaldor J.,
RA Deacon N.;
RT "Characterization of three nef-defective HIV-1 strains associated with
RT long term nonprogression.";
RL J. Virol. 0:0-0(2000).
DR EMBL; AY006000; AAG32143.1; -.
DR HSP; P12520; IDSJ.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.

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DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
SQ SEQUENCE 96 AA; 11346 MW; C1BD60F1048E5036 CRC64;

Query Match 99.2%; Score 252; DB 2; Length 96;
Best Local Similarity 95.9%; Pred. No. 1.4e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 8
ID Q6Q440 PRELIMINARY; PRT; 96 AA.
AC Q6Q440
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Vpr protein.
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Sanchez G.I., Carrion G., Eyzaguirre L., Arias S., Negrete M.,
RA Montano S., Perez J., Russell K.L., Sateren W., Birx D.L., Carr J.K.,
RA Sanchez J.L.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY561244; AAS86190.1; -.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
SQ SEQUENCE 96 AA; 11242 MW; F7893B5D57E14C2C CRC64;

Query Match 98.8%; Score 251; DB 2; Length 96;
Best Local Similarity 95.9%; Pred. No. 1.9e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 49
Db 48 ETYGDWAGVEAIRILQQLLFHFRIGCRHSRIGVTRQRRNGASRS 96

RESULT 9
ID AAS86190 PRELIMINARY; PRT; 96 AA.
AC AAS86190
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Vpr protein.
GN VPR.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCM031;
RA Sanchez G.I., Carrion G., Eyzaguirre L., Arias S., Negrete M.,
RA Montano S., Perez J., Russell K.L., Sateren W., Birx D.L., Carr J.K.,
RA Sanchez J.L.;
RT "Molecular and epidemiological characterization of HIV-1 infected
RT individuals from Medellin, Columbia.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY561244; AAS86190.1; -.
SQ SEQUENCE 96 AA; 11242 MW; F7893B5D57E14C2C CRC64;

Query Match 98.8%; Score 251; DB 2; Length 96;

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Best Local Similarity 95.9%; Pred. No. 1.9e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 48 ETYGDWTAGVGAIIIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96
|||||

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ID VPR_HV1BR STANDARD; PRT; 96 AA.
AC P05928;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, last sequence update)
DE 05-JUL-2004 (Rel. 44, last annotation update)
DE VPR protein (R ORF protein).
GN Names=VPR;
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).
RN [2]
RP SEQUENCE FROM N.A. (CLONE PNL4-3).
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; K02013; AAB59749.1; -.
DR HSSP; P12520; 1BDE.
DR HIV; K02013; VPR$BRU.
DR HIV; M19921; VPR$NL43.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW AIDS.
FT CONFLICT 15 15 H -> Y (in Ref. 2).
FT CONFLICT 28 28 N -> S (in Ref. 2).
FT CONFLICT 41 41 G -> N (in Ref. 2).
FT CONFLICT 85 85 Q -> R (in Ref. 2).
SQ SEQUENCE 96 AA; 11295 MW; 42892A4186583D3E CRC64;

Query Match 98.4%; Score 250; DB 1; Length 96;
Best Local Similarity 98.0%; Pred. No. 2.6e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVGAIIIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
|||||
Db 48 ETYGDWTAGVGAIIIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96
|||||

RESULT 11
Q9IOB8 PRELIMINARY; PRT; 96 AA.
ID Q9IOB8;
AC Q9IOB8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Vpr protein.
GN Names=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20338596; PubMed=10881687;
RA Yamada T., Iwamoto A.;
RT "Comparison of proviral accessory genes between long-term
RT nonprogressors and progressors of human immunodeficiency virus type 1
RT infection.";
RL Arch. Virol. 145:1021-1027(2000).
DR EMBL; AB034527; BAA93974.1; -.
DR HSSP; P12520; 1BDE.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW AIDS.
SQ SEQUENCE 96 AA; 11365 MW; 9EAAF998E0B6DD80 CRC64;

Query Match 98.4%; Score 250; DB 2; Length 96;
Best Local Similarity 95.9%; Pred. No. 2.6e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVGAIIIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
|||||
Db 48 ETYGDWTAGVGAIIIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96
|||||

RESULT 12
VPR_HV1RH STANDARD; PRT; 96 AA.
AC P05954;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, last sequence update)
DT 01-OCT-2004 (Rel. 45, last annotation update)
DE VPR protein (R ORF protein).
GN Name=VPR;
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-staal F.;
RT "Identification and characterization of conserved and variable regions
RT in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";
RL Cell 45:637-648(1986).
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CC -----
DR EMBL; M17451; AAA45055.1; -.
DR PDB; 1F10; NMR; A=12-33.
DR HIV; M17451; VPR$RF.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW 3D-structure; AIDS.
SQ SEQUENCE 96 AA; 11338 MW; 85BC4E4D5CF17741 CRC64;

Query Match 98.0%; Score 249; DB 1; Length 96;
Best Local Similarity 95.9%; Pred. No. 3.6e-26;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETYGDWTAGVGAIIIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 49
|||||
Db 48 ETYGDWTAGVGAIIIRILQQLLFHFRIGCRHSRIGVTRQRRARNGASRS 96
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